

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;; ADDRESSEE: STUART & OLSTEIN
;; STREET: 6 Becker Farm Road
;; CITY: Roseland
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07068
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/07093
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,980
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ferraro, Gregory D.
;; REGISTRATION NUMBER: 36,134
;; REFERENCE/DOCKET NUMBER: 325800-446
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 320 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-07093-2

Query Match 59.7%; Score 968.5; DB 5; Length 320;
Best Local Similarity 59.7%; Pred. No. 1.9e-81;
Matches 178; Conservative 53; Mismatches 66; Indels 1; Gaps 1;

DB 16 ILGLGLEAOWFLAFLPCSLYLVNGLNLTIVYVREHSHHEPMYIFLCMLSGDIL 75
12 VLGIGLEKRAHFWGFPILSTVYVAMCNCIVFTVTERSHAMPTFLCLMAIDLA 71
QY 76 ISTSPKMLATFWNSTTIOPDACLLOMFATHSLSGMESTVLLANAFDRYVAICPLRH 135
72 LSTSPKMLATFWNSTTIOPDACLLOMFATHSLSGMESTVLLANAFDRYVAICPLRH 131
DB 136 ATYTLPRYTKIGVAAVVGALMALPVPFIKQLPFCRSNIISHSYCLHODVKKLACDDT 195
132 AATLANTVVAOIGIVAVVVGSLFFPFLPIKRLAFCHSNVLSHSYCVHODVKKLAVADR 191
QY 196 RVAVVYGLVITISAIGDSLISFSYLLIKTVLIGL-TREAQAKAGTCVSHCAVFIFF 254
192 LPAVNVGLRALILVMGVDMFISLSFLIKTVLQLPSSERKAGTCVSHGVLAFF 251
QY 255 VPIGLSMVHRSKRDSPLVTLANIYLLVPPVNLPIYGVYKTEIRORILFLFVA 312
252 VPIGLSVHRRGNSLHPVRYVMGDIYLLPVPNIPIYGAKTQIRRVYLAFFNIS 309

RESULT 7
US-08-988-876-7
; Sequence 7, Application US/08988876
; Patent No. 6063596
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yoe, Henry
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
; TITLE OF INVENTION: WITH IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: diskette
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/988,876
;; FILING DATE: Herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0441 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 314 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 32086
;; US-08-988-876-7

Query Match 26.6%; Score 431.5; DB 3; Length 314;
Best Local Similarity 34.8%; Pred. No. 3.8e-32;
Matches 109; Conservative 63; Mismatches 120; Indels 21; Gaps 8;

QY 8 NESAATFILIGLGLLEAOWFLAFLPCSLYLVNGLNLTIVYVREHSHHEPMYIFLC 67
5 NQTSISDFLLGLGLEIODEQONLCYALPLAMVLTLLNLTIVIRDSHLPMPYIFLS 64
DB 68 MLGSDILISTSSPKMLATFWNSTTIOPDACLLOMFATHSLSGMESTVLLANAFDRY 127
65 NLSPSDCFESSVTIPKLLQNMQNDPSIPIADCTQMTFLFGDLSFLVMAATRYV 124
QY 128 AICPLHNAVTLPRYTKIGVA--AVVGGALMALPVPFIKQLPFCRSNIISHSYCLH 184
125 AICPLHNAVTLPRYTKIGVA--AVVGGALMALPVPFIKQLPFCRSNIISHSYCLH 181
DB 185 ODVKKLACDDIRN----VYGLIVITISAIGDSLISFSYLLIKTVLIGL-TREAQAK 238
182 SALKIKLAFSTRVNEMVIFIMGLIVT----PFLILISYATVSSILKVPSSKICK 236
QY 239 AFGCVSHVCAVFEYVPIGLSMVHRSKRDSPL-VTLANIYLLVPPVNLPIYGVK 297
237 AFGCVSHVCAVFEYVPIGLSMVHRSKRDSPL-VTLANIYLLVPPVNLPIYGVK 293
DB 298 TKRIRORILRFLH 310
294 NDMKGLSRVTH 306

RESULT 8
US-08-988-876-5
; Sequence 5, Application US/08988876
; Patent No. 6063596
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga

1
2 APPLICANT: Hillman, Jennifer L.
3 APPLICANT: Yue, Henry
4 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
5 TITLE OF INVENTION: WITH IMMUNE RESPONSE
6 NUMBER OF SEQUENCES: 9
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Incyte Pharmaceuticals, Inc.
9 STREET: 3174 Porter Drive
10 CITY: Palo Alto
11 STATE: CA
12 COUNTRY: USA
13 ZIP: 94304
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM Compatible
18 OPERATING SYSTEM: DOS
19 SOFTWARE: PastSeq for Windows Version 2.0
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/988, 876
22 FILING DATE: Herewith
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:
26 FILING DATE:
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Billings, Lucy J.
30 REGISTRATION NUMBER: 36,749
31 REFERENCE/DOCKET NUMBER: PF-0441 US
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 650-855-0555
34 TELEFAX: 650-845-4166
35 TELEX:
36
37 INFORMATION FOR SEQ ID NO: 5:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 309 amino acids
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 IMMEDIATE SOURCE:
44 LIBRARY: GenBank
45 CLONE: 131466/
46
47 US-08-988-876-5

[illegible]

APPLICANT: Lal, Preeti
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
 TITLE OF INVENTION: WITH IMMUNE RESPONSE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0441 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 333 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 205814

	Query Match	23.4%	Score 380;	DB 3;	Length 333;	
	Best Local Similarity	28.0%;	Pred. No. 2.2e-27;			
	Matches	93;	Conservative	74;	Mismatches 133;	Indels 32; Gaps
QY	6	NGNESSATYFLDIGLPGEAEQFWTAAPFCSYLLAVIGNLTIYVYRTHSHHEPMYIF	65			
Db	3	SSNRFRVSEPLLGGVEKKDQLPLTYGLELSMYLVIGNISIIYALISDPCLHPMYMF	62			
QY	66	LCMTSGDILISTSSMPKMLATFWNSSTTIQPDACILQMFALHSLSGMESTVLLANAFDR	125			
Db	63	LSNLSFVDICESTYVPMKLVNIQFQNNVYFAGCITQIYFEFLLEFELDNFLFTIWAYDR	122			
QY	126	YVAICHPRLBNAFVLELP----RYTRIGVAAYVRGAALNAPLRFVFKQDPFCKSNILSHSY	181			
Db	123	YVAICHPMRYVIVIMMYKLCGLGFLVAVSWIVSYLH--ALPQSL--MMIALPFCYHLEPHVF	178			
QY	182	CLHDVYMLACDDIDIVN--VYGLIVIIISALIDSLISFYLLILKTVLGLTR--EAOAK	238			
Db	179	CEPNQVILQSDPAFLNDLVITYFLVLAITYPLAG--IFYSTFKYVSSICAISGHGAK	236			
QY	239	AFGTCVSEVCAVFIFYVDFIGLSMYHRSKRDRSPLPYILANI--YLAVPPVLAIPITYGK	297			
Db	237	AFSTCAHSILSVASLFYCYGLG---YLLSSAANNSSQASATASVMYTVVTPMNPPIYSIKR	293			
QY	298	TKELRQ-----RIILRLRYVATH	314			
Db	294	NKDVAKSVLAKTLCEBIVIRSPSLHFEFLVLCH	325			

Db 241 FSTCSSLVCVGLFSGSAIWMYMAK-SRHEBOQKVLFLIPLSTPMKRP 291

RESULT 12

US-08-465-980-3

Sequence 3, Application US/08465980

Patent No. 5756309

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R.

APPLICANT: LI, YI

APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CROCHT,

ADDRESSEE: STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,980

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-446

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-465-980-3

Query Match 22.3%; Score 361.5; DB 1; Length 247;
Best Local Similarity 36.9%; Pred. No. 7.7e-26;
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

QY 15 FILIGDLEBQWFLAPLCSLYLIVLGNLTIIYVREHSLHEPMTIFLCMSGIDI 74
Db 1 FILIGDLEBQWFLAPLCSLYLIVLGNLTIIYVREHSLHEPMTIFLCMSGIDI 60
QY 75 LISTSMKMLAIFWSTTIQFDACLLQWPAHSLSGMESTVLLAAMDYVAICHLR 134
Db 61 CFSSVTIPKLLQNMQNDPSIPADCLTQMFFLLFGDLESFLVAAAYDXYVAICPL- 119
QY 135 HATVLTLPRTYKIGVA--AVRGAAALMAPLPVFIKQLPFCRSNLSHSCYCIHODVAKLA 191
Db 120 HATVLTLPRTYKIGVA--AVRGAAALMAPLPVFIKQLPFCRSNLSHSCYCIHODVAKLA 177
QY 192 CDDIRVN----VYGLIIVISAIGDLSLSFSYLLILKTVGL-TREAQAKFGTCVS 245
Db 178 FSDTRVNEWVFIWIGGLIIV----PFLILIGSYARIVSILKVPSSKIGCKAFSTGCS 232
QY 246 HVCAPFIYVPEIGL 260
Db 233 HLSVSLFTGTIGL 247

RESULT 13

US-09-053-303-3

Sequence 3, Application US/09053303

Patent No. 5948890

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R.

APPLICANT: LI, YI

APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CROCHT,

ADDRESSEE: STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/053,303

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,980

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-446

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-053-303-3

Query Match 22.3%; Score 361.5; DB 2; Length 247;
Best Local Similarity 36.9%; Pred. No. 7.7e-26;
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

QY 15 FILIGDLEBQWFLAPLCSLYLIVLGNLTIIYVREHSLHEPMTIFLCMSGIDI 74
Db 1 FILIGDLEBQWFLAPLCSLYLIVLGNLTIIYVREHSLHEPMTIFLCMSGIDI 60
QY 75 LISTSMKMLAIFWSTTIQFDACLLQWPAHSLSGMESTVLLAAMDYVAICHLR 134
Db 61 CFSSVTIPKLLQNMQNDPSIPADCLTQMFFLLFGDLESFLVAAAYDXYVAICPL- 119
QY 135 HATVLTLPRTYKIGVA--AVRGAAALMAPLPVFIKQLPFCRSNLSHSCYCIHODVAKLA 191
Db 120 HATVLTLPRTYKIGVA--AVRGAAALMAPLPVFIKQLPFCRSNLSHSCYCIHODVAKLA 177
QY 192 CDDIRVN----VYGLIIVISAIGDLSLSFSYLLILKTVGL-TREAQAKFGTCVS 245
Db 178 FSDTRVNEWVFIWIGGLIIV----PFLILIGSYARIVSILKVPSSKIGCKAFSTGCS 232
QY 246 HVCAPFIYVPEIGL 260
Db 233 HLSVSLFTGTIGL 247

RESULT 14
US-09-339-115-3

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; Sequence 3, Application US/09339115
; Patent No. 6372891
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: LI, YI
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/053,303
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-339-115-3

Query Match 22.3%; Score 361.5; DB 4; Length 247;
Best Local Similarity 36.9%; Pred. No. 7.7e-26;
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

OY 15 FILGLGLEAEQFMALPCLSLYLAVGNLTITIVYREHSLHEPMYIFLCMLSGIDI 74
DB 1 FILGLGLEAEQFMALPCLSLYLAVGNLTITIVYREHSLHEPMYIFLCMLSGIDI 60
OY 75 LISTSSPKMALIFWENSTTIQPDACILQWFAIHSLSGSESTVLLMAFDRYVAICPRLR 134
DB 61 CFSSVTIPKLIQNMQNDPSIPYADCTQWYFLLFGDLESFLLVMAAYDRYVAICPPL- 119
OY 135 HATVLTLPRTKIGVA--AVRGALMALPLVPIKOLPCRSNIIISHSCYCLHODVAKIA 191
DB 120 HYTRIMSPMLCALVALSWLTFTHAMLT--LMAKLCPCADNVIPHFCDMSALAKIA 177
OY 192 CDDIRVN----VYGLIVITISAIGDSLISFSYLLIKTVLGL--TREQAQAFGCVS 245
DB 178 FSDIRVNEWYIFIMGLIIVY-----PFLILISYARIVSILKVPSSKGIKAFSTCGS 232
OY 246 HVCAPFIYVPIGL 260
DB 233 HLSVSLFYGTVIGL 247
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RESULT 15
PCT-US95-07093-3
; Sequence 3, Application PC/TUS9507093
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; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: LI, YI
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,980
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07093-3

Query Match 22.3%; Score 361.5; DB 5; Length 247;
Best Local Similarity 36.9%; Pred. No. 7.7e-26;
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

OY 15 FILGLGLEAEQFMALPCLSLYLAVGNLTITIVYREHSLHEPMYIFLCMLSGIDI 74
DB 1 FILGLGLEAEQFMALPCLSLYLAVGNLTITIVYREHSLHEPMYIFLCMLSGIDI 60
OY 75 LISTSSPKMALIFWENSTTIQPDACILQWFAIHSLSGSESTVLLMAFDRYVAICPRLR 134
DB 61 CFSSVTIPKLIQNMQNDPSIPYADCTQWYFLLFGDLESFLLVMAAYDRYVAICPPL- 119
OY 135 HATVLTLPRTKIGVA--AVRGALMALPLVPIKOLPCRSNIIISHSCYCLHODVAKIA 191
DB 120 HYTRIMSPMLCALVALSWLTFTHAMLT--LMAKLCPCADNVIPHFCDMSALAKIA 177
OY 192 CDDIRVN----VYGLIVITISAIGDSLISFSYLLIKTVLGL--TREQAQAFGCVS 245
DB 178 FSDIRVNEWYIFIMGLIIVY-----PFLILISYARIVSILKVPSSKGIKAFSTCGS 232
OY 246 HVCAPFIYVPIGL 260
DB 233 HLSVSLFYGTVIGL 247
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Job time : 29 secs
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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:58:08 ; Search time 15 seconds

(without alignments)
1244.942 Million cell updates/sec

Title: US-09-966-459A-2

Perfect score: 1623
Sequence: 1 MAMVPNGNSSATFYFILLGL.....KEIRQRIRLRHVATHASRP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCY_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1623	100.0	318 9 US-10-012-896-920	Sequence 920, App
2	1623	100.0	318 9 US-09-895-793-920	Sequence 920, App
3	1623	100.0	318 9 US-09-895-814-920	Sequence 920, App
4	1623	100.0	318 9 US-09-966-459A-2	Sequence 2, Appl1
5	1623	100.0	318 10 US-09-753-143-920	Sequence 920, App
6	1623	100.0	318 10 US-09-780-669-920	Sequence 920, App
7	1623	100.0	318 10 US-09-823-827-920	Sequence 920, App
8	1623	100.0	318 10 US-09-886-055-91	Sequence 91, Appl
9	983	60.6	320 9 US-09-968-033C-4	Sequence 4, Appl1
10	983	60.6	320 9 US-10-012-896-527	Sequence 527, App
11	983	60.6	320 9 US-09-895-793-527	Sequence 527, App
12	983	60.6	320 9 US-09-895-814-527	Sequence 527, App
13	983	60.6	320 10 US-09-759-143-527	Sequence 527, App
14	983	60.6	320 10 US-09-730-018-7	Sequence 7, Appl1
15	983	60.6	320 10 US-09-780-669-527	Sequence 527, App
16	983	60.6	320 10 US-09-823-827-527	Sequence 527, App
17	983	60.6	320 10 US-09-886-055-83	Sequence 83, Appl
18	981	60.4	320 9 US-09-966-459A-12	Sequence 12, Appl
19	969.5	59.7	320 9 US-09-968-033C-2	Sequence 2, Appl1

20	968.5	59.7	320 12 US-10-079-719-2	Sequence 2, Appl1
21	941.5	58.0	324 10 US-09-886-055-81	Sequence 81, Appl
22	892.5	55.0	314 10 US-09-886-055-335	Sequence 335, App
23	872.5	53.8	312 10 US-09-886-055-265	Sequence 265, App
24	845.5	52.1	329 10 US-09-886-055-261	Sequence 261, App
25	828	51.0	317 10 US-09-886-055-93	Sequence 93, Appl
26	827.5	51.0	315 10 US-09-886-055-107	Sequence 107, App
27	820	50.5	319 9 US-09-966-459A-11	Sequence 11, Appl
28	818.5	50.4	314 10 US-09-886-055-85	Sequence 85, Appl
29	818	50.4	313 10 US-09-886-055-115	Sequence 115, App
30	817.5	50.4	314 9 US-10-032-106-10	Sequence 10, Appl
31	817.5	50.4	314 10 US-09-886-055-89	Sequence 89, Appl
32	815	50.2	321 10 US-09-886-055-117	Sequence 117, App
33	815	50.2	321 10 US-09-886-055-259	Sequence 259, App
34	810.5	49.9	314 10 US-09-886-055-263	Sequence 263, App
35	807	49.7	326 9 US-09-966-459A-14	Sequence 14, Appl
36	803	49.5	312 10 US-09-886-055-487	Sequence 487, App
37	802.5	49.4	312 10 US-09-886-055-337	Sequence 337, App
38	800	49.3	302 10 US-09-886-055-337	Sequence 337, App
39	796.5	49.1	318 10 US-09-886-055-101	Sequence 101, App
40	794.5	49.0	324 10 US-09-886-055-219	Sequence 219, App
41	788	48.6	313 10 US-09-886-055-111	Sequence 111, App
42	784	48.3	344 10 US-09-886-055-341	Sequence 341, App
43	782.5	48.2	307 9 US-09-966-459A-9	Sequence 9, Appl1
44	782.5	48.2	326 10 US-09-886-055-267	Sequence 267, App
45	775	47.8	311 10 US-09-886-055-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-10-012-896-920
Sequence 920, Application US/10012896
Publication No. US20020163251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiansheng
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurral, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-896-920

Query Match 100.0%; Score 1623; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.5e-147;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60
DB 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60
QY 61 PMTIFCLMSGIDILISTSSMPKMLAIFWNSSTTIOFDACLLQMPAHSLSGNESTVLLA 120
DB 61 PMTIFCLMSGIDILISTSSMPKMLAIFWNSSTTIOFDACLLQMPAHSLSGNESTVLLA 120
QY 121 MAFDRVVAICHPRLHATVTLPRVTKIGVAAVVGAAALMAPLPEVTKOLPFCRSNLSHS 180
DB 121 MAFDRVVAICHPRLHATVTLPRVTKIGVAAVVGAAALMAPLPEVTKOLPFCRSNLSHS 180
QY 181 YCHADVMKLCDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240
DB 181 YCHADVMKLCDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240
QY 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300
DB 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300
QY 301 IRORIILRFHVATHASEP 318
DB 301 IRORIILRFHVATHASEP 318

RESULT 2

US-09-895-793-920
Sequence 920, Application US/09895793
Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-793-920

Query Match 100.0%; Score 1623; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.5e-147;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60
DB 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60
QY 61 PMTIFCLMSGIDILISTSSMPKMLAIFWNSSTTIOFDACLLQMPAHSLSGNESTVLLA 120
DB 61 PMTIFCLMSGIDILISTSSMPKMLAIFWNSSTTIOFDACLLQMPAHSLSGNESTVLLA 120
QY 121 MAFDRVVAICHPRLHATVTLPRVTKIGVAAVVGAAALMAPLPEVTKOLPFCRSNLSHS 180
DB 121 MAFDRVVAICHPRLHATVTLPRVTKIGVAAVVGAAALMAPLPEVTKOLPFCRSNLSHS 180
QY 181 YCHADVMKLCDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240
DB 181 YCHADVMKLCDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240
QY 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300
DB 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300
QY 301 IRORIILRFHVATHASEP 318
DB 301 IRORIILRFHVATHASEP 318

RESULT 3

US-09-895-814-920
Sequence 920, Application US/09895814
Publication No. US20020193296A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-814-920

Query Match 100.0%; Score 1623; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.5e-147;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60
DB 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60

QY 61 PMTIFLCMLSGIDILISTSSMPKMLAFMFNSTTIOFDACILQMFALHSLSGMESTVLLA 120
DB 61 PMTIFLCMLSGIDILISTSSMPKMLAFMFNSTTIOFDACILQMFALHSLSGMESTVLLA 120
QY 121 MAFDRYAICHPLRHATVTLPRYTKIGVAAYVGAALMAPLPFIRKOLPFCRSNIIISHS 180
DB 121 MAFDRYAICHPLRHATVTLPRYTKIGVAAYVGAALMAPLPFIRKOLPFCRSNIIISHS 180
QY 181 YCLHODVWKLACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240
DB 181 YCLHODVWKLACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVEIFVYFPGLSMVRHRSKRSDPLPYILANIYLLVPPVLPNIVGVKTKRE 300
DB 241 GTCVSHCAVEIFVYFPGLSMVRHRSKRSDPLPYILANIYLLVPPVLPNIVGVKTKRE 300
QY 301 IRORIILRFHVATHASEP 318
DB 301 IRORIILRFHVATHASEP 318

RESULT 4
US-09-966-459a-2
Sequence 2, Application US/09966459A
Publication No. US2003002237A1

GENERAL INFORMATION:

APPLICANT: FEDER, J.N.
APPLICANT: MINTIER, G.
APPLICANT: RAMANATHAN, C.S.
APPLICANT: HAKKEN, D.R.
APPLICANT: CACACE, A.
APPLICANT: BARBER, L.
APPLICANT: KORNACKER, M.G.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HSPRBYT4,
FILE REFERENCE: D0039NP
CURRENT APPLICATION NUMBER: US/09/966,459A
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,833
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/261,776
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/305,351
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/313,202
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-459a-2

Query Match 100.0%; Score 1623; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.5e-147;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFDRYAICHPLRHATVTLPRYTKIGVAAYVGAALMAPLPFIRKOLPFCRSNIIISHS 180
DB 1 MAFDRYAICHPLRHATVTLPRYTKIGVAAYVGAALMAPLPFIRKOLPFCRSNIIISHS 180
QY 181 YCLHODVWKLACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240
DB 181 YCLHODVWKLACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240

QY 241 GTCVSHCAVEIFVYFPGLSMVRHRSKRSDPLPYILANIYLLVPPVLPNIVGVKTKRE 300
DB 241 GTCVSHCAVEIFVYFPGLSMVRHRSKRSDPLPYILANIYLLVPPVLPNIVGVKTKRE 300
QY 301 IRORIILRFHVATHASEP 318
DB 301 IRORIILRFHVATHASEP 318

RESULT 5
US-09-759-143-920
Sequence 920, Application US/09759143
Patent No. US20020022248A1

GENERAL INFORMATION:

APPLICANT: Xu, JIANGCHUN
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-143-920

Query Match 100.0%; Score 1623; DB 10; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.5e-147;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFDRYAICHPLRHATVTLPRYTKIGVAAYVGAALMAPLPFIRKOLPFCRSNIIISHS 180
DB 1 MAFDRYAICHPLRHATVTLPRYTKIGVAAYVGAALMAPLPFIRKOLPFCRSNIIISHS 180
QY 181 YCLHODVWKLACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240
DB 181 YCLHODVWKLACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVEIFVYFPGLSMVRHRSKRSDPLPYILANIYLLVPPVLPNIVGVKTKRE 300
DB 241 GTCVSHCAVEIFVYFPGLSMVRHRSKRSDPLPYILANIYLLVPPVLPNIVGVKTKRE 300
QY 301 IRORIILRFHVATHASEP 318
DB 301 IRORIILRFHVATHASEP 318

RESULT 6

US-09-780-669-920

; Sequence 920, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqun

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Panger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darriek

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Ajun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepier, William

; APPLICANT: Hurai, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 920

; LENGTH: 318

; TYPE: PRF

; ORGANISM: Homo sapiens

; US-09-780-669-920

Query Match 100.0%; Score 1623; DB 10; Length 318;

Best Local Similarity 100.0%; Pred. No. 2.5e-147;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDPNNGESSATYFTILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60
 DB 1 MAMDPNNGESSATYFTILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60
 QY 61 PNTIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHISLGSNESTVLA 120
 DB 61 PNTIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHISLGSNESTVLA 120
 QY 121 MAMDRTVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCNSNLSHS 180
 DB 121 MAMDRTVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCNSNLSHS 180
 QY 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLLKTVLGLTREAQKAF 240
 DB 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLLKTVLGLTREAQKAF 240
 QY 241 GTCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYLANIYLLVPPVLPPIYGVATKE 300
 DB 241 GTCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYLANIYLLVPPVLPPIYGVATKE 300
 QY 301 IRORIILRFHVAATHASEP 318
 DB 301 IRORIILRFHVAATHASEP 318

RESULT 7

US-09-822-827-920

; Sequence 920, Application US/09822827

; Patent No. US20020081680A1

; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.534C1
 ; CURRENT APPLICATION NUMBER: US/09/822,827
 ; CURRENT FILING DATE: 2001-03-28
 ; NUMBER OF SEQ ID NOS: 982
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 920
 ; LENGTH: 318
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 ; US-09-822-827-920

Query Match 100.0%; Score 1623; DB 10; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2.5e-147;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDPNNGESSATYFTILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60
 DB 1 MAMDPNNGESSATYFTILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60
 QY 61 PNTIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHISLGSNESTVLA 120
 DB 61 PNTIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHISLGSNESTVLA 120
 QY 121 MAMDRTVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCNSNLSHS 180
 DB 121 MAMDRTVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCNSNLSHS 180
 QY 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLLKTVLGLTREAQKAF 240
 DB 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLLKTVLGLTREAQKAF 240
 QY 241 GTCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYLANIYLLVPPVLPPIYGVATKE 300
 DB 241 GTCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYLANIYLLVPPVLPPIYGVATKE 300
 QY 301 IRORIILRFHVAATHASEP 318
 DB 301 IRORIILRFHVAATHASEP 318

RESULT 8

US-09-886-055-91

; Sequence 91, Application US/09886055

; Patent No. US20020132273A1

; GENERAL INFORMATION:

; APPLICANT: STRYER, LUBERT

; APPLICANT: ZOZULYA, SERGEY

; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND

; FILE REFERENCE: 078003-0277150

; CURRENT APPLICATION NUMBER: US/09/886,055

; CURRENT FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: 60/213,812

; PRIOR FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 522

; SOFTWARE: patentin ver. 2.1

; SEQ ID NO 91

; LENGTH: 318

; TYPE: PRF

; ORGANISM: Homo sapiens

; US-09-886-055-91

Query Match 100.0%; Score 1623; DB 10; Length 318;

Best Local Similarity 100.0%; Pred. No. 2.5e-147;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDPNNGESSATYFTILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60
 DB 1 MAMDPNNGESSATYFTILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60

QY 61 PATIFLCMISGIDILISTSSMPKMLAIFWENSTTIOFDACILQMFALHSISGMSFVILA 120
 DB 61 PATIFLCMISGIDILISTSSMPKMLAIFWENSTTIOFDACILQMFALHSISGMSFVILA 120
 QY 121 MADRVATACHPRLHNAVTLPRVTKIGVAAVVRGAALMAPLVEFKQDFPCRSNLSHS 180
 DB 121 MADRVATACHPRLHNAVTLPRVTKIGVAAVVRGAALMAPLVEFKQDFPCRSNLSHS 180
 QY 181 YCHADVMKACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGLTREDAQAKF 240
 DB 181 YCHADVMKACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGLTREDAQAKF 240
 QY 241 GPCVSHVCAVFIFYPFISGMSVHRSKRSDPLVILANITVLLVPVLPNIYGVKTE 300
 DB 241 GPCVSHVCAVFIFYPFISGMSVHRSKRSDPLVILANITVLLVPVLPNIYGVKTE 300
 QY 301 IRORIILFEVATHASEP 318
 DB 301 IRORIILFEVATHASEP 318

RESULT 9
 US-09-966-033C-4
 ; Sequence 4, Application US/09968033C
 ; Patent No. US2002016871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet et al.
 ; TITLE OF INVENTION: Human Prostate Specific G-Protein Receptor HPRMJ70
 ; FILE REFERENCE: PFI80P1
 ; CURRENT APPLICATION NUMBER: US/09/968,033C
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,275
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 09/339,115
 ; PRIOR FILING DATE: 1999-06-24
 ; PRIOR APPLICATION NUMBER: 09/053,303
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 08/465,980
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-966-033C-4

Query Match 60.6%; Score 983; DB 9; Length 320;
 Best Local Similarity 59.8%; Pred. No. 3, 2e-86;
 Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESATYFLLIGLPGLEAQFNLAPPLCSLYLAVGNLTITTYVREHSLHEPMTFLC 67
 DB 5 NETHAT-FVLIGLPGLEKAFHWGFPPLSMYVAMGNCIVAEIVTERSLHAPMTFLC 63
 QY 68 MLSGIDILISTSSMPKMLAIFWENSTTIOFDACILQMFALHSISGMSFVILAMADRVY 127
 DB 64 MLAIDALSTSMKRLALFWDSEISREACTQWFFIHALSAESTILLAMADRVY 123
 QY 128 AICHPRLHNAVTLPRVTKIGVAAVVRGAALMAPLVEFKQDFPCRSNLSHSYCHQDV 187
 DB 124 AICHPRLHNAVTLPRVTKIGVAAVVRGAALMAPLVEFKQDFPCRSNLSHSYCHQDV 183
 QY 188 MKLACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGL-TREDAQAKFGTCVSH 246
 DB 184 MKLAVADTLPRNVVYGLTALVWGVDVMTLSYFLIRIVQLPSKSERAKAFGTCVSH 243
 QY 247 VCAVFIFYPFISGMSVHRSKRSDPLVILANITVLLVPVLPNIYGVKTEIRORIL 306
 DB 244 IGVVLAFFVPLILSLSVHREGNSLHPIRVVMGDITLLPVIINPITYGAKTKOIRTVL 303
 QY 307 RLEFHA 312
 DB 307 RLEFHA 312

DB 304 AMFKIS 309

RESULT 10
 US-10-012-896-527
 ; Sequence 527, Application US/10012896
 ; Publication No. US20020183251A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Ketter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skelky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hurl, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Mantabe, Yoshihiro
 ; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427027
 ; CURRENT APPLICATION NUMBER: US/10/012,896
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 1011
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 527
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-012-896-527

Query Match 60.6%; Score 983; DB 9; Length 320;
 Best Local Similarity 59.8%; Pred. No. 3, 2e-86;
 Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESATYFLLIGLPGLEAQFNLAPPLCSLYLAVGNLTITTYVREHSLHEPMTFLC 67
 DB 5 NETHAT-FVLIGLPGLEKAFHWGFPPLSMYVAMGNCIVAEIVTERSLHAPMTFLC 63
 QY 68 MLSGIDILISTSSMPKMLAIFWENSTTIOFDACILQMFALHSISGMSFVILAMADRVY 127
 DB 64 MLAIDALSTSMKRLALFWDSEISREACTQWFFIHALSAESTILLAMADRVY 123
 QY 128 AICHPRLHNAVTLPRVTKIGVAAVVRGAALMAPLVEFKQDFPCRSNLSHSYCHQDV 187
 DB 124 AICHPRLHNAVTLPRVTKIGVAAVVRGAALMAPLVEFKQDFPCRSNLSHSYCHQDV 183
 QY 188 MKLACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGL-TREDAQAKFGTCVSH 246
 DB 184 MKLAVADTLPRNVVYGLTALVWGVDVMTLSYFLIRIVQLPSKSERAKAFGTCVSH 243
 QY 247 VCAVFIFYPFISGMSVHRSKRSDPLVILANITVLLVPVLPNIYGVKTEIRORIL 306
 DB 244 IGVVLAFFVPLILSLSVHREGNSLHPIRVVMGDITLLPVIINPITYGAKTKOIRTVL 303
 QY 307 RLEFHA 312
 DB 304 AMFKIS 309

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C3
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-143-527

Query Match 60.6%; Score 983; DB 10; Length 320;
Best Local Similarity 59.8%; Pred. No. 3.2e-86;
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESAATYFLLIGLPGLEAOWFLAPLCSLYIANVGNLTIYYRTSHSHRPYILC 67
DB 5 NETAAT-FVLIGIPGLEAHEFWGFPILSMYVAMFGNCIYFIVTERSLHAPYILC 63
QY 68 MLSGIDILISTSMKMLAIFWENSTTIOFDACLQMFHISLGSVESTVLLAMAFDRY 127
DB 64 MIAADLALSTMKILATFWDSREISFEACLOMFHIALSIESTIILAMAFDRY 123
QY 128 AICHELRAAVLTLPRTKIGVAAVNGAALAPLPEIKOLPECRSNILSHSYCLHODV 187
DB 124 AICHELRAAVLTLPRTKIGVAAVNGAALAPLPEIKOLPECRSNILSHSYCLHODV 183
QY 188 MKIACDDIRVNVVGLIYIISAGLSLISPSYLLIKTYGL-TREAAKAFGTCVSH 246
DB 184 MKIADADLPNVVGLIYIISAGLSLISPSYLLIKTYGL-TREAAKAFGTCVSH 243
QY 247 VCAVEFYVPFGLSMVRFKRSRSDPLVILANLYLLVPLNPIVGVKKEIRORIL 306
DB 244 IGVVLAFTVPLIGLSVHFRGNSLRPIYRVWGDYLLPLPINIIGAKTKOIRTVL 303
QY 307 RLPHVA 312
DB 304 AMFKIS 309

RESULT 14
US-09-730-018-7
Sequence 7, Application US/09730018
Patent No. US2002004877A1
GENERAL INFORMATION:
APPLICANT: All, Shujath
APPLICANT: Calferkey, Robert
APPLICANT: Recipon, Heve
APPLICANT: Sun, Yonnging
TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and
FILE REFERENCE: Treating Prostate Cancer
CURRENT APPLICATION NUMBER: US/09/730, 018
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/169,083
PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-09-730-018-7

Query Match 60.6%; Score 983; DB 10; Length 320;
Best Local Similarity 59.8%; Pred. No. 3.2e-86;
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESAATYFLLIGLPGLEAOWFLAPLCSLYIANVGNLTIYYRTSHSHRPYILC 67
DB 5 NETAAT-FVLIGIPGLEAHEFWGFPILSMYVAMFGNCIYFIVTERSLHAPYILC 63
QY 68 MLSGIDILISTSMKMLAIFWENSTTIOFDACLQMFHISLGSVESTVLLAMAFDRY 127
DB 64 MIAADLALSTMKILATFWDSREISFEACLOMFHIALSIESTIILAMAFDRY 123
QY 128 AICHELRAAVLTLPRTKIGVAAVNGAALAPLPEIKOLPECRSNILSHSYCLHODV 187
DB 124 AICHELRAAVLTLPRTKIGVAAVNGAALAPLPEIKOLPECRSNILSHSYCLHODV 183
QY 188 MKIACDDIRVNVVGLIYIISAGLSLISPSYLLIKTYGL-TREAAKAFGTCVSH 246
DB 184 MKIADADLPNVVGLIYIISAGLSLISPSYLLIKTYGL-TREAAKAFGTCVSH 243
QY 247 VCAVEFYVPFGLSMVRFKRSRSDPLVILANLYLLVPLNPIVGVKKEIRORIL 306
DB 244 IGVVLAFTVPLIGLSVHFRGNSLRPIYRVWGDYLLPLPINIIGAKTKOIRTVL 303
QY 307 RLPHVA 312
DB 304 AMFKIS 309

RESULT 15
US-09-780-669-527
Sequence 527, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillio, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/780, 669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens

US-09-780-669-527

Query Match

60.6%; Score 983; DB 10; Length 320;

Best Local Similarity 59.8%; Pred. No. 3, 2e-86; Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

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QY 8 NESSATVFILIGLPGLEAQMFLAPLPCSLYLAVGNLTIIYIVREHSLHEPMYFLC 67
   | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 5 NETHAT FVLIGLPGLEKAFMWGFFLLSMYVAMFGNCIVAFIVKERSLHAPMILFLC 63
   || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 68 MMSGIDILISTSSMPKMLAFENSTTIQDACLQMFALHSLSGMESTVLLAMAFDRY 127
   || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 64 MLAIDIALSTSMPKILAFWDSREISFEACLTQMFIFHALSAIESITLLAMAFDRY 123
   || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 128 AICHPLRHATVTLPRVTKIGAAVVRGAAALMAPLVYFIKQLPCKSNIIISHSYCLHODY 187
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 124 AICHPLRHAALVNTVTAQIGIYAVVRGSLFFEPPLPLIKRLAFCHSNVLSHSYCVHODY 183
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 188 MKLACODIRVNVYVGLIVISATIGDSLISFSYLILKTVLGL-TREAQAKAFGTCVSH 246
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 184 MKLAVADTLPRNVYGLTALILVMGVDMFISLSFELIRIVLQLPSKSERAKAFGTCVSH 243
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 247 VCAVFIFYVPEIGLSMVRFSKRSDSPLPYILANITYLLVPPVLPVYGVYKTEIRORIL 306
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 244 IGVYLAIFYVPLIGLSVYHRFGNSLHPIVRVYMGDIYLLRPVINPIYGAKTQIRFRVL 303
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 307 RLEHVA 312
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 304 AMFKIS 309
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
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Search completed: March 26, 2003, 10:05:08
Job time : 16 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:53:07 ; Search time: 46 Seconds
(without alignments)
664.581 Million cell updates/sec

Title: US-09-966-459a-2

Sequence: 1 KMVDPNGNSATYFILGL.....KEIRKRLRLFNHATASEP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	33.9	292	2 A60547	hypothetical prote
2	477.5	29.4	313	2 E45774	odorant receptor 8
3	453	27.9	307	2 S29710	olfactory receptor
4	440	27.1	312	2 A46247	olfactory receptor
5	434.5	26.8	312	2 I23701	olfactory receptor
6	434.5	26.8	319	2 JC5624	olfactory receptor
7	433.5	26.7	312	2 S29708	olfactory receptor
8	432	26.6	328	2 G45774	odorant receptor 2
9	431.5	26.6	310	2 E23701	olfactory receptor
10	431.5	26.6	314	2 S20572	olfactory receptor
11	425.5	26.2	314	2 A37286	olfactory receptor
12	424.5	26.2	321	2 H45774	odorant receptor 3
13	422.5	26.0	305	2 S29711	olfactory factor 0
14	420.5	25.9	314	2 S29707	olfactory receptor
15	418.5	25.8	309	1 S51356	odorant receptor 1
16	415	25.6	344	2 I45774	olfactory receptor 1
17	413	25.4	312	2 A48413	probable olfactory
18	411.5	25.4	311	2 JC5300	chemoreceptor TB33
19	411	25.3	160	2 S58066	probable olfactory
20	411	25.3	313	2 S20571	olfactory receptor
21	406.5	25.0	311	2 C23701	olfactory receptor
22	405	25.0	317	2 F45774	odorant receptor 4
23	404.5	24.9	313	2 B23701	olfactory receptor
24	401.5	24.7	312	2 G23701	olfactory receptor
25	399.5	24.6	314	2 H23701	olfactory receptor
26	399.5	24.6	328	2 A45774	odorant receptor 3
27	399.5	24.6	328	2 D45774	odorant receptor 3
28	397.5	24.5	328	2 B45774	odorant receptor 3
29	394.5	24.3	320	2 S20573	olfactory receptor

30	393.5	24.2	316	2 A57069	olfactory receptor
31	388.5	23.9	315	2 JC5836	olfactory receptor
32	387.5	23.9	328	2 C45774	odorant receptor 3
33	386.5	23.8	304	2 S29709	olfactory receptor
34	386.5	23.8	312	2 A46750	olfactory receptor
35	380	23.4	333	2 A23701	olfactory receptor
36	379.5	23.4	337	2 F23701	olfactory receptor
37	379	23.4	317	2 D23701	olfactory receptor
38	371.5	22.9	315	2 JC4658	olfactory receptor
39	370	22.8	315	2 JC5201	chemoreceptor TB56
40	366	22.6	318	2 JC5202	chemoreceptor TB64
41	310.5	19.1	222	2 B40745	odorant receptor (
42	310.5	19.1	234	2 S29000	g protein-coupled
43	307.5	18.9	264	2 PC4369	olfactory receptor
44	289.5	17.8	234	2 S28999	g protein-coupled
45	285.5	17.6	222	2 D40745	odorant receptor (

ALIGNMENTS

RESULT 1

A60547 hypothetical protein (HPFH breakpoint 3' region) - human (fragment)

N:Alternate names: Olfactory receptor homolog

C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence, revision 17-Apr-1993 #text_change 26-Aug-1999

C:Accession: A60547; A60482

R:Reingold, E.A.; Forget, B.G.

Blood 74, 2178-2186, 1989
A:Title: The breakpoint of a large deletion causing hereditary persistence of fetal

A:Reference number: A60547, MID:90028751, PMID:2478223

A:Molecule type: DNA
A:Residues: 1-292 <FE1>

C:Superfamily: olfactory receptor OR14

Query Match 33.9%; Score 551; DB 2; Length 292;

Best local Similarity 41.0%; Pred. No. 1.8e-41;
Matches 114; Conservative 50; Mismatches 92; Indels 22; Gaps 6;

QY	17	LIGLPGLEAOFMLAPFLCSLYLAVLGNLTIVYTERSHLEPNTIFCLMSGIDILI	76
DB	29	LVGIPGLSEVQCNIQIDPFCALYILAMIGNSLISIKERSLHEPITIFLNGATGATIAL	88
QY	77	STSGMPMLAIFPENS-TTIOFDACLOMFAIR-SLSGMSYVLLAMAFRYAICPLR	134
DB	89	ASSIMPEMLGYSGLMCKLSILIPAC---FNVVPHINGIESGILVAMADRYVAICYPLR	145
QY	135	HATVTLPRYTKIGVAVAVGALMLAPLVEIK-QLPFCNSLISHSYCLHGVNKLACD	193
DB	146	HANIFHQVLIQIGTMVNLAAATLVAPCHVILICRQVFYHTVISHSYCHEMAIVKLA	205
QY	194	DIRNVVYGLIIVISAIGDSLISFSLILKTVLGL-TREAQAKFGCVSHCAVFI	252
DB	206	NGVYMKRYGLFVAFYVAGPFLFTLSYIQIFITVFRLPKRKARFAPNCINAHICVFO	265
QY	253	FVYPIGLSMVHRKRRDSPLVILLANYLVLPVVLN	290
DB	266	FYLLAFSFTTHRGSH-----IPVYIH	288

RESULT 2

E45774 odorant receptor 8 - channel catfish

C:Species: Ictalurus punctatus (channel catfish)
C>Date: 20-Feb-1995 #sequence, revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: E45774
R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993
A:Title: The family of genes encoding odorant receptors in the channel catfish.

A:Reference number: A45774; MID:93201590; PMID:7916654
A:Accession: E45774

Query Match 26.8%; Score 434.5; DB 2; Length 312;
 Best Local Similarity 33.5%; Pred. No. 4.4e-31;
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;

OY 8 NESAATYFLLGLPGLAEQFWLAFPLCSLYLAVNGNLTYITVREHSLHEPMTYELC 67
 DB 5 NQTVISQFLGLGLPPEEHLFLFALFLAVLFTIIGNLITIVRLDSHLMHPMYELTS 64

OY 68 MLSGIDILISTSSMPKMLAFWFRSTTIQDACLQMFALHSLSGNESTVLLAMAFDRY 127
 DB 65 NLSGSDLCFSSVMPKLLQNMQSOVPSISTYGCLOTQYFFWFGDMSEFLVYVAYDXRV 124

OY 128 AICHPHRAVTLTPRYTKIGVAAYV-----RGALMAPLPVPIKOLPFCRSNLISHSY 181
 DB 125 AICPPLATYIMS-----TKCASLYLLMLMTHTALHTL--LIARLSFEKNTILHFE 178

OY 182 CLHODVKLACDDIRVN-----VYGLIYIISAIGDLSLISFSLYLKTVLGL-TRBA 235
 DB 179 CDISALTKLCSIDYVNEIMTYIGLIIIT-----PFLIIVMSYVRIFFSILKFPSTIQD 233

OY 236 QARAFGCVSHCAVFFIYFPIGLSMVHRFSKRDSPLPITANIYLLVPPVLPPIYVG 295
 DB 234 IYKVFSTGSHLSVTLFYGITIGIYLCF--SGNMSTVKELAMAMVTVVPMNPFIYS 291

OY 296 VKTEIRORILRL 308
 DB 292 LRNDKRALIRV 304

RESULT 6
 olfactory receptor HTRPC92 - human
 JC5624
 C/Species: Homo sapiens (man)
 C/Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 20-Jun-2000
 C/Accession: J05624; S58003
 R/Vanderheggen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
 Blochem. Biophys. Res. Commun. 237, 283-287, 1997
 A/Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed
 A/Reference number: J05624; M01D:97415789; PMID:9268701
 A/Contents: Testis
 A/Accession: J05624
 A/Molecule type: mRNA
 A/Residues: 1-319 <RAN>
 A/Cross-references: GB:Y10530; NID:g7792017; PIDN:CAA71558.1; PID:g7792018
 R/Vanderheggen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
 Submitted to the EMBL Data Library, July 1995
 A/Description: Male germ cells from several mammalian species express a specific repertoire
 A/Reference number: S57995
 A/Accession: S58003
 A/Molecule type: mRNA
 A/Residues: 126-282 <VAM>
 A/Cross-references: EMBL:X89677; NID:g902337; PIDN:CAA61824.1; PID:g902338
 C/Genetics:
 A/Map position: 19p13.1
 C/Function:
 A/Description: Involved in control of sperm physiology
 C/Superfamily: olfactory receptor OR14
 C/Keywords: G protein-coupled receptor; transmembrane protein
 F/36-48/Domain: transmembrane #status predicted <TM1>
 F/38-79/Domain: transmembrane #status predicted <TM2>
 F/101-120/Domain: transmembrane #status predicted <TM3>
 F/140-164/Domain: transmembrane #status predicted <TM4>
 F/197-218/Domain: transmembrane #status predicted <TM5>
 F/237-260/Domain: transmembrane #status predicted <TM6>
 F/272-292/Domain: transmembrane #status predicted <TM7>

Query Match 26.8%; Score 434.5; DB 2; Length 319;
 Best Local Similarity 33.7%; Pred. No. 4.5e-31;
 Matches 103; Conservative 70; Mismatches 118; Indels 15; Gaps 8;

OY 7 GNESAATYFLLGLPGLAEQFWLAFPLCSLYLAVNGNLTYITVREHSLHEPMTY 63
 DB 4 GNTQVISEFLGLPSPGRGLPFLGL---FLSNVLTVAGNLLIATISDSHLHPMY 60

OY 64 IFCLSLSGIDILISTSSMPKMLAFWFRSTTIQDACLQMFALHSLSGNESTVLLAMAF 123
 DB 61 FFLSLNSPADLCVSTSTIPKMLMTIQNKYITVITACLMQWFFILRAGFENFLLSVAY 120

OY 124 DRYVACHPHRAVTLTPRYTKIGVAAYVVGALMAPLP-ETKOLPFCRSNLISHSYC 182
 DB 121 DRYVACHPHRAVTLTPRYTKIGVAAYVVGALMAPLP-ETKOLPFCRSNLISHSYC 179

OY 183 LHQDVKLACDDIRVN-----VYGLIYIISAIGDLSLISFSLYLKTVLGL-TRBAQAKA 239
 DB 180 ELNGLVQLACSDSPFLNHVYFTVALGGLPLTGL-YSYKLISSIHAISSAQGYKA 237

OY 240 FGTGVSHCAVFFIYFPIGLSMVHRFSKRDSPLPITANIYLLVPPVLPPIYVG 299
 DB 238 FSTGSHLSVSLFYGITIGIYLCF--SANTRNSSSAPAVYVTVVPMNPFIYSLNR 295

OY 300 EIRORILRL 305
 DB 296 DIKRAL 301

RESULT 7
 S29708
 olfactory receptor OR12 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C/Accession: S29708
 R/Ramling, K.; Krieger, J.; Strothmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.;
 Nature 361, 353-356, 1993
 A/Title: Cloning and expression of odorant receptors.
 A/Reference number: S29707; M01D:93149273; PMID:7678922
 A/Accession: S29708
 A/Molecule type: mRNA
 A/Residues: 1-312 <RAN>
 C/Superfamily: olfactory receptor OR14

Query Match 26.7%; Score 433.5; DB 2; Length 312;
 Best Local Similarity 32.0%; Pred. No. 5.4e-31;
 Matches 99; Conservative 74; Mismatches 119; Indels 17; Gaps 6;

OY 8 NESAATYFLLGLPGLAEQFWLAFPLCSLYLAVNGNLTYITVREHSLHEPMTY 65
 DB 5 NQTVISQFLGLGLPPEEHLFLFALFLAVLFTIIGNLITIVRLDSHLMHPMYELTS 62

OY 66 MLSGIDILISTSSMPKMLAFWFRSTTIQDACLQMFALHSLSGNESTVLLAMAFDR 125
 DB 63 NLSGSDLCFSSVMPKLLQNMQSOVPSISTYGCLOTQYFFWFGDMSEFLVYVAYDXRV 122

OY 126 YVATCHPRAVTLTPRYTKIGVAAYVVGALMAPLP-ETKOLPFCRSNLISHSYC 185
 DB 123 YVATCHPRAVTLTPRYTKIGVAAYVVGALMAPLP-ETKOLPFCRSNLISHSYC 182

OY 186 DVNKLACDDIRVN-----VYGLIYIISAIGDLSLISFSLYLKTVLGL-TRBAQAKA 239
 DB 183 DVNKLACDDIRVN-----VYGLIYIISAIGDLSLISFSLYLKTVLGL-TRBAQAKA 237

OY 240 FGTGVSHCAVFFIYFPIGLSMVHRFSKRDSPLPITANIYLLVPPVLPPIYVG 299
 DB 238 FSTGSHLSVSLFYGITIGIYLCF--SANTRNSSSAPAVYVTVVPMNPFIYSLNR 295

OY 300 EIRORILRL 308
 DB 296 DIKRAL 304

RESULT 8
 G45774
 odorant receptor 202 - channel catfish
 C/Species: Ictalurus punctatus (channel catfish)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998
 C/Accession: G45774
 R/Mat, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

A:status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-314 <RUC>
 A:Cross-references: GB:M64392; MID:q205845; PIDN:AAA1755.1; PID:q205846
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.2%; Score 425.5; DB 2; Length 314;
 Best Local Similarity 33.2%; Pred. No. 2.8e-30;
 Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;

8 NESATVFILIGLPGLEAQQ-FMLAPPLCSILYLANGLTIYVTEHSLSHEPKYIF 65
 DB 5 NQVYISQFLLELPPISEHOFVYALF-LSMTITVYLGMLITLITLHDSHATPPYLF 62
 QY 66 LCMISGIDILISTSMKPMALFENSTTIQDACLQMFALHISLSGMESTVLLAMAFDR 125
 DB 63 LSNLSFSDLCFSSVTMKLQNNQSVPSIPFAGCLQQLFYLYKALDESEFLVMAAYDR 122
 QY 126 YVAICHPRLAATVLTLPRTKIGVAAVNGAALM--APL-PVFIKOLPFCRSNITLSHY 181
 DB 123 YVAICHPRLAATVLTLPRTKIGVAAVNGAALM--APL-PVFIKOLPFCRSNITLSHY 178
 QY 182 CLADQVAKLACDDIRVN-----VYGLVITISAGLDSLISPSYLLIKTVGL-TREA 235
 DB 179 CDSPLPLAKSCDPRHVELYFVAGGLVYIPYV-----LIIVSYANVAVSILKVPESVKG 233
 QY 236 QAAAFGCVSHVCAVFIFYVPIGLSNVHRFSKRDSPLPVILANIYLLVPPVNIPIYVG 295
 DB 234 IHRIFSGSGSHLSVSLFETIIGLYLCP--SANNSTVKETVAMMYTAVTPMLNPPIYS 291
 QY 296 VKTEIRORLRL 308
 DB 292 LRNDKMEALIRV 304

RESULT 12

45774
 odorant receptor 3 - channel catfish
 C:Species: Ictalurus punctatus (channel catfish)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998
 C:Accession: H45774

R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.
 Cell 72, 657-666, 1993
 A:Title: The family of genes encoding odorant receptors in the channel catfish.
 A:Reference number: H45774; MID:93201350; PMID:7916654

A:status: preliminary; not compared with conceptual translation
 A:Accession: H45774
 A:Molecule type: mRNA
 A:Residues: 1-321 <NGA>

A:Experimental source: olfactory epithelium
 A:Note: Sequence extracted from NCB1 backbone (NCBIP:127745)
 C:Superfamily: olfactory receptor OR14
 C:Keywords: olfaction; transmembrane protein

Query Match 26.2%; Score 424.5; DB 2; Length 321;
 Best Local Similarity 32.7%; Pred. No. 3.5e-30;
 Matches 102; Conservative 68; Mismatches 127; Indels 15; Gaps 6;

10 SSATV-----FILIGLPGLEAQMFLAPPLCSYLIVANGLTIYVTEHSLSHEPMYI 64
 DB 14 TMTFTFRSPFYITGLYNIPHAKYTLF-LCFYTVTFELGNSPFGITVILARSLHTAKYI 72
 QY 65 FLMLSGIDILISTSMKPMALFENSTTIQDACLQMFALHISLSGMESTVLLAMAFDR 124
 DB 73 AVNMLASDLCGSSALPKLIDMLLEFNOSISYEACSNMFYVCFWTLQCLFLLALAYD 132
 QY 125 RYVAICHPRLAATVLTLPRTKIGVAAVNGAALMPLPVFIKOLPFCRSNITLSHSCILH 184
 DB 133 RLTAICHPRLAATVLTLPRTKIGVAAVNGAALMPLPVFIKOLPFCRSNITLSHSCILH 192
 QY 185 QDVAKLACDDIRVN---VYGLVITISAGLDSLISPSYLLI-LKTVGLTREDAQAKAF 240

DB 193 GPIYKACNDNTINSIMGNVCTAILLPILLITIASYICGFALOKIARGV---EQYKAM 249
 QY 241 GCVSHVCAVFIFYVPIGLSNVHRFSKRDSPLPVILANIYLLVPPVNIPIYVG 300
 DB 250 KTCSHLLVAMFYLPIISVTV-ALTTRIDTNIRIINFALQIFPPLNPIIYATKEE 308
 QY 301 IRQRIQLRF-HV 311
 DB 309 VMOAKIKLLYKH 320

RESULT 13

529711
 olfactory factor OR37 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C:Accession: S29711

R:Ramng, K.; Krieger, J.; Strotmann, J.; Boehhoff, I.; Kudlick, S.; Baumstark, C.; I
 Nature 361, 353-356, 1993
 A:Title: Cloning and expression of odorant receptors.
 A:Reference number: S29707; MID:93149273; PMID:7678922

A:Accession: S29711
 A:Molecule type: mRNA
 A:Residues: 1-305 <RAM>
 C:Superfamily: olfactory receptor OR14

Query Match 26.0%; Score 422.5; DB 2; Length 305;
 Best Local Similarity 32.8%; Pred. No. 5e-30;
 Matches 101; Conservative 61; Mismatches 115; Indels 31; Gaps 5;

16 ILIGLPGLEAQMFLAPPLCSYLIVANGLTIYVTEHSLSHEPMYIFLCMSGIDIL 75
 DB 1 LILGSGPKTEILYFVILVAVLTHGNGVLITASIFDSHLTPMTFFGNLSFLDIC 60
 QY 76 ISTSMKPMALFENSTTIQDACLQMFALHISLSGMESTVLLAMAFDRVYALCHPLRH 135
 DB 61 YTTSSVPSTIVSLSKRNISFSGCTQMFVGFANGSTECILGMARDVYALCHPLRY 120
 QY 136 ATVLTLPRTKI-----GVAAVNGAALMPLPVFIKOLPFCRSNITLSHY 187
 DB 121 SVMSKEYVYMASASWFSGINSVYQTSIAM-----RLPFGNNVNIHFTCEVLAV 172
 QY 188 MKLACDDIRVN---VYGLVITISAGLDSLISPSYLLIKTVGL-TREAQAFGCVSH 246
 DB 173 LKLMACDILNIVWVNIWVNMALFVLPILITFFSYLLITLRMSASGRRKASTCSAH 232
 QY 247 VCAVFIFYVPIGLSNVHRFSKRDSPL-----PVILANIYLLVPPVNIPIYVG 297
 DB 233 LTVVVFETGIFSM-----YAKPKSQDLTGDKPQTSKIISLFGVGYTPMLNPPIYSIR 287
 QY 298 TKEIRORI 305
 DB 288 NKDVAAV 295

RESULT 14

529707
 olfactory receptor OR5 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
 C:Accession: S29707; B37286

R:Ramng, K.; Krieger, J.; Strotmann, J.; Boehhoff, I.; Kudlick, S.; Baumstark, C.; I
 Nature 361, 353-356, 1993
 A:Title: Cloning and expression of odorant receptors.
 A:Reference number: S29707; MID:93149273; PMID:7678922

A:Accession: S29707
 A:Molecule type: mRNA
 A:Residues: 1-314 <RAM>
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991

A:Title: A novel multigene family may encode odorant receptors: a molecular basis for
 A:Reference number: A23701; MID:91191556; PMID:1840504
 A:Accession: B37286

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:48:21 ; Search time 25 seconds

(without alignments)
527.379 Million cell updates/sec

Title: US-09-966-459a-2

Perfect score: 1623

Sequence: 1 MMVDNGNSATYFIILGL.....KEIRRIILTFVATVHASEP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	983	60.6	320	1	OXE2_HUMAN
2	981	60.4	320	1	OXE2_RAT
3	872.5	53.8	312	1	OX12_HUMAN
4	810.5	49.9	314	1	OX11_HUMAN
5	796.5	49.1	318	1	OYD1_HUMAN
6	778.5	48.0	315	1	OXM1_HUMAN
7	763	47.0	317	1	OYR2_HUMAN
8	755	46.5	312	1	OYR1_HUMAN
9	728.5	44.9	312	1	OXB2_HUMAN
10	708	43.6	313	1	OYB6_HUMAN
11	633	39.0	310	1	OXB4_HUMAN
12	468	28.8	319	1	O2S2_HUMAN
13	440	27.1	312	1	OL15_MOUSE
14	435.5	26.8	314	1	O5F1_HUMAN
15	434.5	26.8	312	1	OLF4_RAT
16	434.5	26.6	319	1	O7A5_HUMAN
17	432.5	26.6	312	1	O2C1_HUMAN
18	431.5	26.6	310	1	OLF0_RAT
19	431	26.6	314	1	OLF1_HUMAN
20	431	26.6	323	1	OLF1_HUMAN
21	430	26.5	315	1	OLF1_RAT
22	428.5	26.4	311	1	OA42_HUMAN
23	428	26.4	312	1	OLF3_CANFA
24	427.5	26.3	312	1	OLF1_HUMAN
25	426.5	26.3	315	1	OB41_HUMAN
26	425.5	26.2	314	1	OLF1_RAT
27	425	26.2	317	1	OA45_HUMAN
28	423.5	26.1	321	1	O5V1_HUMAN
29	422.5	26.0	320	1	O7C1_HUMAN
30	421	25.9	317	1	O2F1_HUMAN
31	420.5	25.9	312	1	OLF6_CHICK
32	420.5	25.9	313	1	OLF1_HUMAN
33	420.5	25.9	314	1	OA43_HUMAN

34	418	25.8	311	1	O5P3_HUMAN	OBW294 homo sapien
35	415.5	25.6	312	1	OLF4_CHICK	P37070 gallus gall
36	413.5	25.5	311	1	O2J3_HUMAN	O76001 homo sapien
37	413	25.4	312	1	O1D2_HUMAN	P34987 homo sapien
38	412.5	25.4	318	1	OLF1_CHICK	P37067 gallus gall
39	411.5	25.3	311	1	O8B8_HUMAN	O15620 homo sapien
40	411	25.3	311	1	OLF1_CANFA	O95154 canis famli
41	411	25.3	313	1	OLF0_CANFA	P30955 canis famli
42	411	25.3	318	1	OAHL_HUMAN	O9Y488 homo sapien
43	410	25.3	309	1	O5B2_HUMAN	O96709 homo sapien
44	409.5	25.2	313	1	O2B6_HUMAN	P58173 homo sapien
45	409.5	25.2	313	1	OLF5_RAT	P23266 rattus norv

ALIGNMENTS

RESULT 1
OXE2_HUMAN
ID OXE2_HUMAN STANDARD; PRT; 320 AA.
AC 09H255;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor)
DE (HPRM).
GN OR51E2 OR PSGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21002538; PubMed-11118034;
RA Xu L.L., Stackhouse B.G., Florence K., Zhang W., Shanmugam N.,
RA Sesterhenn I.A., You Z., Srikantan V., Augustus M., Roschke V.,
RA Carter K., McLeod D.G., Moui J.W., Soppet D., Srivastava S.;
RT "PSGR, a novel prostate-specific gene with homology to a G
RT protein-coupled receptor, is overexpressed in prostate cancer.";
RL Cancer Res. 60:6568-6572(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21564169; PubMed-11707321;
RA Yuan T.T., Toy P., McClary J.A., Lin R.J., Miyamoto N.G.,
RA Kretschmer P.J.;
RT "Cloning and genetic characterization of an evolutionarily conserved
RT human olfactory receptor that is differentially expressed across
RT species.";
RL Gene 278:41-51(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE-Prostate;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN THE PROSTATE.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: AF311306; AAG40776.1; -
DR EMBL: AF369708; AAK38728.1; -
DR EMBL: AF033942; AAK37530.1; -
DR EMBL: BC020768; AAK20768.1; -
DR Genew: HGNC:15195; ORS152.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR000237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 23
FT TRANSMEM 24 48
FT DOMAIN 49 59
FT TRANSMEM 60 84
FT DOMAIN 85 100
FT TRANSMEM 101 119
FT DOMAIN 120 142
FT TRANSMEM 143 162
FT TRANSMEM 163 197
FT TRANSMEM 198 221
FT DOMAIN 222 235
FT TRANSMEM 236 260
FT DOMAIN 261 292
FT TRANSMEM 293 320
FT DISULFID 96 178
FT CARBOHYD 5 5
SQ SEQUENCE 320 AA; 35492 MW; 03582CC2AAB6E2C6 CRC64;

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Query Match Best Local Similarity 59.8%; Score 983; DB 1; Length 320;

Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

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QY 8 NEESSATYFLILGPGLEAOFMLAPLCSLYLIYAVGNTLIYIVTERSLHEPMTIFLC 67
DB 5 NEEHAT-FVLIGIPGLEAKHFVGPFLLSMYVAMGNCIVAYIVTERSLHAPMTIFLC 63
QY 68 MNSGDIILSTSMRKALIFWNSITTOFDACILOMFAHISGSESYVLAMADRY 127
DB 64 MLAALDIALSTMPKILALFWDSREITFDALOMFTHALSAESTITLAMADRY 123
QY 128 AICHPLRHATVLTLPRTKIGVAAVVGAAALMAPLVFKOLPFCNSNLSHSCYCHODV 187
DB 124 AICHPLRHAAVLTNTYQIGVAAVVGSLFFPPLIKRLAFCSNLSHSCYCHODV 183
QY 188 MLIACDDIRNVVYGLVITSAIGDLSLISFSYLLIKTVGL-TREAQAKAFGTCVSH 246
DB 184 MLIATVDLTPNVYGLTALILVWGVDVMTISLSTYFLIIRTVGLPESKSRARAFGTCVSH 243
QY 247 VCAVPLEFYVPIGLSVNHRFSKRSDPLPYLIANTYLLVPVLPVLPVYGVTKREIKRQL 306
DB 244 IGVYLAFTVPLIGLSVNHRSGLDPIYVAVMGDVTLLPVPVLPVLPVYGVTKRQITRVL 303
QY 307 RLEHVA 312
DB 304 AMEKIS 309

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RESULT 2

OXE2_RAT OXE2_RAT STANDARD; PRT; 320 AA.

```

AC 088628;
DR 16-OCT-2001 (Rel. 40; Created)
DR 16-OCT-2001 (Rel. 40; Last sequence update)
DR 16-OCT-2001 (Rel. 40; Last annotation update)
DE Olfactory receptor 5122 (G-protein coupled receptor RALc).
GN ORS152.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99131082; PubMed=9932290;
RA Raming K., Konzelmann S., Breer H.;
RT Identification of a novel G-protein coupled receptor expressed in
RT distinct brain regions and a defined olfactory zone.;
RL Recept. Channels 6:141-151(1998).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN SOME AREAS OF THE BRAIN AND
CC IN THE OLFACTORY EPITHELIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sdb.ch).
CC
CC EMBL: AF079864; AAD12761.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC
CC PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 23
FT TRANSMEM 24 48
FT DOMAIN 49 59
FT TRANSMEM 60 84
FT DOMAIN 85 119
FT TRANSMEM 120 138
FT TRANSMEM 139 162
FT TRANSMEM 163 197
FT TRANSMEM 198 221
FT TRANSMEM 222 235
FT TRANSMEM 236 260
FT DOMAIN 261 292
FT TRANSMEM 293 320
FT DISULFID 96 178
FT CARBOHYD 5 5
SQ SEQUENCE 320 AA; 35505 MW; E7F78F5F5D5B94 CRC64;

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Query Match Best Local Similarity 59.8%; Score 981; DB 1; Length 320;

Matches 183; Conservative 52; Mismatches 69; Indels 2; Gaps 2;

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QY 8 NEESSATYFLILGPGLEAOFMLAPLCSLYLIYAVGNTLIYIVTERSLHEPMTIFLC 67
DB 5 NEEHAT-FVLIGIPGLEAKHFVGPFLLSMYVAMGNCIVAYIVTERSLHAPMTIFLC 63
QY 68 MNSGDIILSTSMRKALIFWNSITTOFDACILOMFAHISGSESYVLAMADRY 127
DB 64 MLAALDIALSTMPKILALFWDSREITFDALOMFTHALSAESTITLAMADRY 123
QY 128 AICHPLRHATVLTLPRTKIGVAAVVGAAALMAPLVFKOLPFCNSNLSHSCYCHODV 187
DB 124 AICHPLRHAAVLTNTYQIGVAAVVGSLFFPPLIKRLAFCSNLSHSCYCHODV 183
QY 188 MLIACDDIRNVVYGLVITSAIGDLSLISFSYLLIKTVGL-TREAQAKAFGTCVSH 246
DB 184 MLIATVDLTPNVYGLTALILVWGVDVMTISLSTYFLIIRTVGLPESKSRARAFGTCVSH 243
QY 247 VCAVPLEFYVPIGLSVNHRFSKRSDPLPYLIANTYLLVPVLPVLPVYGVTKREIKRQL 306
DB 244 IGVYLAFTVPLIGLSVNHRSGLDPIYVAVMGDVTLLPVPVLPVLPVYGVTKRQITRVL 303
QY 307 RLEHVA 312
DB 304 AMEKIS 309

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DB 304 AMFKIS 309

RESULT 3

OX12_HUMAN STANDARD; PRT; 312 AA.

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Olfactory receptor 5112 (HORS/beta12).

OR5112.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

SEQUENCE FROM N.A.

MEDLINE=20570519; PubMed=11121057;

Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M., Felsenfeld G., Groudine M., Hardison R.;

Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta-globin gene clusters.

Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).

-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL: AF137396; AAC41678.1;

InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1. 1.

DR PRINTS: PR00237; GPCR_Rhodopsn.

DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.

DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 26 49 1 (POTENTIAL).

FT TRANSMEM 50 57 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 58 79 2 (POTENTIAL).

FT TRANSMEM 80 100 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 101 120 3 (POTENTIAL).

FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 140 158 4 (POTENTIAL).

FT TRANSMEM 159 195 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 196 219 5 (POTENTIAL).

FT TRANSMEM 220 236 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 237 259 6 (POTENTIAL).

FT TRANSMEM 260 268 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 275 294 7 (POTENTIAL).

FT TRANSMEM 295 312 CYTOPLASMIC (POTENTIAL).

FT DISULFID 97 189 BY SIMILARITY.

FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).

SEQUENCE 312 AA; 35002 MW; F17CD16C95FD1AF6 CRC64;

Query Match 53.8%; Score 872.5; DB 1; Length 312;

Best Local Similarity 53.9%; Pred. No. 3.4e-59;

Matches 164; Conservative 50; Mismatches 89; Indels 1; Gaps 1;

DB 8 NNSAFYPLTGLPGLERAGFLAPPLCLVLAIVGNTIYIYRTESLHPMTIFLC 67

DB 5 NTHPAFFLLTIPGLSSHWSLGLCVAVAGNVIIQAARVPSLHPMTYFLS 64

QY 68 MLSGDILISTSMKMLAIFWNTTIOFDACLLQMFALHSLGMSVLLAMADRY 127

DB 65 MFSFVAISMATLPYLRFPCLANRITFDALIQEFLHFFSMMSGILLAMSEFRV 124

QY 128 AICHPLEHATVTLPRYTKIGAAVVRGAALAPLPYFIKQDPGCSNIISSYCLHODY 187

DB 125 AICDPLRATVATVTEVLAAGLGAARSFTLEPLLRRLRDLCHSNVLSHSYCLPDM 184

QY 188 MKLACDIDIRNVVYGLVITISAIIGDLSLFSFVITLTKVIG-LTREQAKAPGCVSH 246

DB 185 MKLACDIDISNITGLVSTFGMDLFFTLSTVLILSVMTASREERLALNTCVSH 244

QY 247 VCAVFTFYVPEIGLSVWHRFSKRDRSPLPYILANILVLPVLPYGVKTEIRORIL 306

DB 245 ILAVLAFYVPMIGVSIVHRGKAVPCIVHLMENVTLPVPLIYSKTEIRAIRF 304

QY 307 RLPH 310

DB 305 RMFH 308

RESULT 4

OX12_HUMAN STANDARD; PRT; 314 AA.

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Olfactory receptor 5111 (HORS/beta11).

OR5111.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

SEQUENCE FROM N.A.

MEDLINE=20570519; PubMed=11121057;

Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M., Felsenfeld G., Groudine M., Hardison R.;

Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta-globin gene clusters.

Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).

-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL: AF137396; AAC41679.1;

InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1. 1.

DR PRINTS: PR00237; GPCR_Rhodopsn.

DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.

DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.

KW G-protein coupled receptor; Transmembrane;

KW Multigene family; Olfaction.

FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 28 51 1 (POTENTIAL).

FT TRANSMEM 52 59 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 60 81 2 (POTENTIAL).

FT TRANSMEM 82 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 122 3 (POTENTIAL).

FT TRANSMEM 123 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 160 4 (POTENTIAL).

FT TRANSMEM 161 197 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 198 221 5 (POTENTIAL).

FT TRANSMEM 222 238 CYTOPLASMIC (POTENTIAL).

TRANSMEM 239 261 6 (POTENTIAL).
 FT DOMAIN 262 270 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 277 296 7 (POTENTIAL).
 FT DOMAIN 297 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 99 191 BY SIMILARITY.
 SQ SEQUENCE 314 AA; 35483 MW; 08B40AD9C894911 CRC64;

Query Match 49.98; Score 810.5; DB 1; Length 314;
 Best Local Similarity 48.78; Pred. No. 1,7e-54;
 Matches 151; Conservative 65; Mismatches 93; Indels 1; Gaps 1;

QY 2 MVDNNGSSATYFILLGLPGLEAOFWLAFLPCLSLVLAIVGNLTIIYVTEHSLEP 61
 DB 1 MGLNGPPPPATQLGIGPGLTGLTVALIFCLIMISTISLTLFWEPALHOP 60
 QY 62 MYIFCLMISGIDILISTSSPKMLAIFWNSTTIOFDACILOMFAHSLSGNESTVLLAM 121
 DB 61 MYIFCLMISGIDILISTSSPKMLAIFWNSTTIOFDACILOMFAHSLSGNESTVLLAM 120
 QY 122 AFDRTVAICPLRAATVLTLPRTKIGVAAVYRGAAALAPLPVFIKQLPFCRSNLTSHSY 181
 DB 121 SLDRFVALCYPLRYVYLTNHRILAMGIGITKSPFTLPPEPFVYKRLPFCGNVLAHSY 180
 QY 182 CLHODVMLACDDIRVNVYGLVITSAIGDSLISFSTLLIKTVLG-LTREAOAKAF 240
 DB 181 CLHODVMLACDDIRVNVYGLVITSAIGDSLISFSTLLIKTVLG-LTREAOAKAF 240
 QY 241 GCVSHVCAVFIYVPPVIGLSMVRHSKRDPPLVPIIANIYLLVPPVLPVYGVYKKE 300
 DB 241 NTCSHICAVAFYVPIIYAVSMIRHFWKSAPVYVYVMSNYLFPPLNPIIYSVKKE 300
 QY 301 IRQRLIRLFH 310
 DB 301 IRKGLKFEH 310

RESULT 5
 OYDL_HUMAN STANDARD; PRT; 318 AA.
 AC 09H346;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 52D1 (HORS/beta14).

GN OR52D1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20570519; PubMed-11121057;
 RA Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,
 RA Felsenfeld G., Grondine M., Hardison R.;
 RT "Comparative structural and functional analysis of the olfactory
 RT receptor genes flanking the human and mouse beta-globin gene
 RT clusters.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

DR EMBL: AF137396; AAC61676.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.

FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 52 1 (POTENTIAL).
 FT DOMAIN 53 60 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 61 82 2 (POTENTIAL).
 FT DOMAIN 83 103 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 104 123 3 (POTENTIAL).
 FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 143 161 4 (POTENTIAL).
 FT DOMAIN 162 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 222 5 (POTENTIAL).
 FT DOMAIN 223 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 262 6 (POTENTIAL).
 FT DOMAIN 263 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 298 7 (POTENTIAL).
 FT DISULFID 299 318 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 100 192 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 318 AA; 35121 MW; 17896807D613C82 CRC64;

Query Match 49.18; Score 796.5; DB 1; Length 318;
 Best Local Similarity 46.58; Pred. No. 1.9e-53;
 Matches 146; Conservative 70; Mismatches 93; Indels 5; Gaps 4;

QY 2 MVDPN-GSSSATYFILLGLPGLEAOFWLAFLPCLSLVLAIVGNLTIIYVTEHSLEH 59
 DB 1 MDSNLSNHLPTFF-LGIGLEPLRAHWIAPPCATVIALVGNALIVANDNLH 59
 QY 60 EPMYIFCLMISGIDILISTSSPKMLAIFWNSTTIOFDACILOMFAHSLSGNESTVLL 119
 DB 60 APMYIFCLMISGIDILISTSSPKMLAIFWNSTTIOFDACILOMFAHSLSGNESTVLL 119
 QY 120 AAFDRYVAICPLRAATVLTLPRTKIGVAAVYRGAAALAPLPVFIKQLPFCRSNLTSH 179
 DB 120 AAFDRYVAICPLRAATVLTLPRTKIGVAAVYRGAAALAPLPVFIKQLPFCRSNLTSH 179
 QY 180 SYCLHODVMLACDDIRVNVYGLVITSAIGDSLISFSTLLIKTVLG-LTREAOAK 238
 DB 180 TYCEHNGIARLACAMITVNIYVGLVALLAMGDSILAIISGFLIHAVHLPSSDAOK 239
 QY 239 AFGCVSHVCAVFIYVPPVIGLSMVRHSKR-DSPVPIIANIYLLVPPVLPVYGVYK 297
 DB 240 ALSTGSHGILIVYIPAFESFELTHRGHNPVHIFLANTLVLPVLPNPIIYGAR 299
 QY 298 TREIRQRLIRLFH 311
 DB 300 TREIRSRLLKLHL 313

RESULT 6
 OYDL_HUMAN STANDARD; PRT; 315 AA.
 AC 09H341;

DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Olfactory receptor 51M1 (HORS/beta7).

GN OR51M1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20570519; PubMed-11121057;
 RA Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,
 RA Felsenfeld G., Grondine M., Hardison R.;
 RT "Comparative structural and functional analysis of the olfactory
 RT receptor genes flanking the human and mouse beta-globin gene

RT clusters.;

RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: AF137396; AAC41681.1; ALT. INIT.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSIN.

DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 27 50 1 (POTENTIAL).

FT TRANSSEM 51 58 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 59 80 2 (POTENTIAL).

FT TRANSSEM 81 101 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 102 121 3 (POTENTIAL).

FT TRANSSEM 122 140 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 141 159 4 (POTENTIAL).

FT TRANSSEM 160 196 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 197 220 5 (POTENTIAL).

FT TRANSSEM 221 237 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 238 260 6 (POTENTIAL).

FT TRANSSEM 261 275 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 276 295 7 (POTENTIAL).

FT TRANSSEM 296 315 CYTOPLASMIC (POTENTIAL).

FT DISULFID 98 190 BY SIMILARITY.

FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 315 AA; 35462 MW; DC19D2F5456D2005 CRC64;

Query Match 48.0%; Score 778.5; DB 1; Length 315;

Best Local Similarity 47.8%; Pred. No. 4,4e-52;

Matches 141; Conservative 64; Mismatches 89; Indels 1; Gaps 1;

QY 15 FILGLGLEAEQWLAFLPLCSLYLAVGNLTIIYVREHSHHEMYTFLCMLSGIDI 74

DB 13 FILSPGLBGLKIMIFIPFFMTMAISGCFILIIKINPRILATPMYLLSLATLDTL 72

QY 75 LISTSPKMLAIFWPNSTTIOFDACILQMFALHSLSGMESTVLLAMAFDRVAICHLR 134

DB 73 GLCVSTLPTMGITFNPSSQSIYFACQIOFCHISFSPMESTVLLAMSFDFVAICHLR 132

QY 135 HATVLTLPRTKIGVAANVRGAALMADLPVFIKQLPFCRSNIILSHSYCLHODVKLACDD 194

DB 133 YSVIITGQVVRAGLIYIFRGPAVITIPYLLIKAFPGYGSVLSHSCPLHQEVIQLACTD 192

QY 195 IRVNVVGLIYIISAIGDSLISFSTLLIKTYLGL-TREAQAKAGTCVSHCAVPIF 253

DB 193 TTFNNKLGAMVVTVMIDVLLALSTGLILHTVAGLASDEORRARTOTCAHRCACAVLVE 252

QY 254 YVPFGLSMVHRSKRSDSPPLVILANITYLLVPPVLANIYVGVTKETRIORIL 308

DB 253 FVPFMGLSLVHRFGKAPRAIHLMANVYLFVPMPLNPIITISIKTEIHRATIKL 307

RESULT 7

OYB2_HUMAN STANDARD; PRT; 317 AA.

AC Q96RD2;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Olfactory receptor 52B2.

GN OR52B2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE OF 70-287 FROM N.A.

RA Fuchs T., Malecova B., Linhart C., Sharan R., Khan M., Herwig R.,

RA Simulovich D., Eikon R., Steinfach M., O'Brien J.K., Radcliff U.,

RA Leinbach H., Olander Z., Glusman G., Lancet D., Shamir R.,

RT "DEFOC: a practical scheme for deciphering families of genes."

RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

DR EMBL: AF399505; AK94990.1;

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 28 51 1 (POTENTIAL).

FT TRANSSEM 52 59 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 60 81 2 (POTENTIAL).

FT TRANSSEM 82 102 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 103 122 3 (POTENTIAL).

FT TRANSSEM 123 141 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 142 160 4 (POTENTIAL).

FT TRANSSEM 161 197 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 198 221 5 (POTENTIAL).

FT TRANSSEM 222 238 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 239 261 6 (POTENTIAL).

FT TRANSSEM 262 276 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 277 296 7 (POTENTIAL).

FT TRANSSEM 297 317 CYTOPLASMIC (POTENTIAL).

FT DISULFID 99 191 BY SIMILARITY.

FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 317 AA; 35642 MW; DB17DB8791F85E21 CRC64;

Query Match 47.0%; Score 763; DB 1; Length 317;

Best Local Similarity 49.2%; Pred. No. 6.5e-51;

Matches 148; Conservative 57; Mismatches 94; Indels 2; Gaps 2;

QY 15 FILGLGLEAEQWLAFLPLCSLYLAVGNLTIIYVREHSHHEMYTFLCMLSGIDI 74

DB 14 FVLPGIPLEAHVHMLSTPCLIVITVNGSILIVYVNERNLAVPYFFLSMAVMDI 73

QY 75 LISTSPKMLAIFWPNSTTIOFDACILQMFALHSLSGMESTVLLAMAFDRVAICHLR 134

DB 74 LISTTVKALAIEMIQAHNIAFDACVQGFVHMEFGESAILLAMAFFRVAICHLR 133

QY 135 HATVLTLPRTKIGVAANVRGAALMADLPVFIKQLPFCRSNIILSHSYCLHODVKLACDD 194

DB 134 YTVVTPVVRGIALAVTRSFCLIFPILKRIPLCTVNIIVPSYEHGIVANLACDD 193

QY 195 IRVNVVGLIYIISAIGDSLISFSTLLIKTYLGL-TREAQAKAGTCVSHCAVPIF 253

DB 194 ITVINWGFSPYPIYAVILDLIVANSYLILRAVFRPSQARHKAALSTGSHLCVILMF 253

QY 254 YVPFGLSMVHRSKRSDSPPLVILANITYLLVPPVLANIYVGVTKETRIORIL-RLFVYA 312

DB 254 YVPSEFTLTHHFRGNIPQVHIIILANLYVAVPPMLNPIYVGVTKQIRREGVAHREFDIK 313

OY	313 T 313
Db	314 T 314
<hr/>	
RESULT 8	
ID	OVAL_HUMAN
AC	OVAL
DT	16-OCT-2001 (Rel. 40, Created)
D7	16-Oct-2001 (Rel. 40, Last sequence update)
D7	16-Oct-2001 (Rel. 40, Last annotation update)
DE	Olfactory receptor 52A1 (HPFHIOF) (HOR3/beta4).
GN	OR52A1.
OS	Homo sapiens (Human).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEMLINE-99443868; PubMed=10512676;
RT	Felngold E.A., Penny L.A., Nienhuis A.W., Forget B.G.;
RT	*An olfactory receptor gene is located in the extended human beta-
RT	globin gene cluster and is expressed in erythroid cells.*;
RL	Genomics 61:15-23(1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEMLINE-20570519; PubMed=11121057;
RA	Bulger M., Bender M.A., van Doornick J.H., Wertman B., Farrell C.M.,
RA	Palsenfeld G., Groudine M., Hardison R.;
RT	*Comparative structural and functional analysis of the olfactory
RT	receptor genes flanking the human and mouse beta-globin gene
RT	clusters.*;
RC	Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
CL	-I- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-I- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration -
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CC	use by non-profit institutions as long as its content is in no way
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@sib-sib.ch).
CC	-----
DR	EMBL; AF154673; AAD51279.1; -
DR	EMBL; AF289204; AAG42367.1; -
DR	GeneW; HGNC:8318; OR52A1.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm.1; 1.
DR	PRINTS; PR00037; GPCRHOOPS.
DR	PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
DR	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Multi-gene family; Olfaction.
FT	DOMAIN 1 27
FT	TRANSMEM 28 51
FT	DOMAIN 52 59
FT	TRANSMEM 60 81
FT	DOMAIN 82 102
FT	TRANSMEM 103 122
FT	DOMAIN 123 141
FT	TRANSMEM 142 160
FT	DOMAIN 161 198
FT	TRANSMEM 199 222
FT	DOMAIN 223 239
FT	TRANSMEM 240 262
FT	DOMAIN 263 271
FT	TRANSMEM 278 297
FT	DOMAIN 298 312
FT	DISULFD 99 182
FT	EXTRACELLULAR (POTENTIAL). 1 (POTENTIAL). 2 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 3 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL). 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL). EXTRACELLULAR (POTENTIAL). 7 (POTENTIAL). CYTOPLASMIC (POTENTIAL). BY SIMILARITY.

```

FT CARBOHYD 5 5 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 312 AA; 35332 MM; B3A92379552D513C CRC64;

Query Match 46.5%; Score 755; DB 1; Length 312;
Best Local Similarity 48.1%; Pred. No. 2.6e-50;
Matches 142; Conservative 57; Mismatches 94; Indels 2; Gaps 2.

Oy 17 LIGLGLAEAPFIAFLPCSTLYLVANLNTFIYVTRFESHHEPMYIFPLMGSDILIT 76
Db 16 LVGIGLGLSVQWCWIGIPFCATILIMIGNSLLSTIKERSLHEPIYIFLGLGATDIAL 75
Oy 77 STSSPKMLAIFWENSTTIQEDACLLOFPAHSLSGMESTVILLAMADRYVAICPLRHA 136
Db 76 ASSIPKMLGIFWENVPEIYEDSCLOMFIHTTLOGISGIVAAALNRYVAICPYLRA 135
Oy 137 TVLPLPRTKIGVAAVVGALMAPLPEIFK-QLPEFCSNLTSHSYCYLHODVWKLACDII 195
Db 136 NIFTHQVLVIGTMVLLAAILVACVLVLCRQFPIHTYTSYCEHMAIVKLAANV 195
Oy 196 RVNVVYGLIVITISAIGLDSLISFSLYLILKLTIGL-TREDAKAGFCVSHVCAVFIY 254
Db 196 QVNRKYGLEFVAVTAVGFLTFITLSYIQIFIVFRLPQKFAKFNACIHAICVFLQY 255
Oy 255 VPIGLSNVHFESKRSDPLVIILANITLVLPVNPVLYGVKTEIRORILRF 309
Db 256 LIAFSEFTTHRGSHIPIYIHTLSFSTYLLVPPINPLVIGAKTYQIRLHVVMF 310

RESULT 9
OXB2_HUMAN
ID OXB2_HUMAN STANDARD; PRT; 312 AA.
AC Q9Y5PI; Q96RD4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Olfactory receptor 51B2 (HORS/beta3).
GN OR51B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-99238494; PubMed-10220430;
RA Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.,
RA Bender M.A., Felsenfeld G., Axel R., Groudine M.,
RT "Conservation of sequence and structure flanking the mouse and human
RT beta-globin loci: the beta-globin genes are embedded within an array
RT of odorant receptor genes."
RL Proc. Natl. Acad. Sci. U.S.A. 96:5129-5134(1999).
RP [2]
RN ERBAYDN.
RP Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.,
RA Bender M.A., Felsenfeld G., Axel R., Groudine M.;
RL Proc. Natl. Acad. Sci. U.S.A. 96:8307-8307(1999).
RL [3]
RP SEQUENCE OF 66-283 FROM N.A.
RA Fuchs T., Malecova B., Linhart C., Sharan R., Rhen M., Herzig R.,
RA Stimuljevich D., Eikon R., Steinfath M., O'Brien J.R., Kadelof U.,
RA Lehrbach A., Glender Z., Glusman G., Lancet D., Shamir R.,
RT "DEBOG: a practical scheme for deciphering families of genes."
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC EMBL: AF137396; AAD29425.2;
DR EMBL: AF399503; AAK94988.1;
DR Genew: HGNC:14703; ORS1B2.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1.1.
DR PRINTS: PS00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECP.F1.1.
DR PROSITE: PS00262; G_PROTEIN_RECP.F1.2; 1.
DR G-protein coupled receptor; Transmembrane; glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 24 47 1 (POTENTIAL).
FT DOMAIN 48 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 77 2 (POTENTIAL).
FT DOMAIN 78 98 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 99 118 3 (POTENTIAL).
FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 138 156 4 (POTENTIAL).
FT DOMAIN 157 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 217 5 (POTENTIAL).
FT DOMAIN 218 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 257 6 (POTENTIAL).
FT DOMAIN 258 266 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 292 7 (POTENTIAL).
FT DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).
FT DISULFID 95 187 BY SIMILARITY.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 312 AA; 35513 MW; 0DA1160267778BDD CRC64;

Query Match 44.9%; Score 728.5; DB 1; Length 312;
Best Local Similarity 44.1%; Pred. No. 2.6e-48;
Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1;

OY 11 SATFTILGLPGLEAOFWLAFLPLCSLYLAVAGNTIIVTSHLEPPTFLCMS 70
DB 6 TAAPELTFEPGLEAHHHISIPFPAVYVCIILGNGMLTLIRHDSLHPPTFTLMLA 65
OY 71 GDILSTSMRMLAIFWNSSTIOFDACLLQMFALHSHSGMESTVILMAFDRAVAC 130
DB 66 GDULMTLTTPVGMILWVNHREISSVGCFLDAFTFHSVSGSLMLMAYDRFAIR 125
OY 131 HPLRAHATVLTLPRTKIGVAANVRGAALMAPLPVFIKQLPFCSNLSHSCYCHODVMKL 190
DB 126 NPLRAVSIITNRVIALGVFIRAGFVSILPVILRFESFYCKSHVITRAFCLHQEIMRL 185
OY 191 ACDDIVANVYGLIYIISAIGDSLISFYLILKTVGL-TREAOAKAFGCVSHVCA 249
DB 186 ACADIFENFLYPVILSLITFLDSLILFESYIILMTLVIGIASGEERAKALNTCISHISC 245
OY 250 VLFETVYFGLSNVHRSKRSDPLVILANTILNVPVNPVYGVKTEIKRIQLRL 308
DB 246 VLFETVYFGLSNVHRSKRSDPLVILANTILNVPVNPVYGVKTEIKRIQLRL 304

RESULT 10
OY6_HUMAN STANDARD; PRT; 313 AA.
AC Q96RD3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Olfactory receptor 52b6.
GN OR52B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 70-287 FROM N.A.
RA Fuchs T., Malecova B., Linhart C., Shayan R., Khen M., Herwig R.,
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Redelof U.,
RA Lehrach H., Olender Z., Glusman G., Lancet D., Shamir R.;

```

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RT DEPOG: a practical scheme for deciphering families of genes.*;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL: AF399504; AAK94989.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1.1.
DR PROSITE: PS00237; G_PROTEIN_RECP.F1.1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP.F1.2; 1.
DR G-protein coupled receptor; Transmembrane; glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 51 1 (POTENTIAL).
FT DOMAIN 52 59 2 (POTENTIAL).
FT TRANSMEM 60 81 2 (POTENTIAL).
FT DOMAIN 82 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 160 4 (POTENTIAL).
FT DOMAIN 161 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 220 5 (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 260 6 (POTENTIAL).
FT DOMAIN 261 295 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 295 7 (POTENTIAL).
FT DOMAIN 296 313 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 313 AA; 35523 MW; 6FC174BDDC20B83 CRC64;

Query Match 43.6%; Score 708; DB 1; Length 313;
Best Local Similarity 43.2%; Pred. No. 9.2e-47;
Matches 140; Conservative 56; Mismatches 112; Indels 2; Gaps 2;

OY 6 NNESSATYFILGLPGLEAOFWLAFLPLCSLYLAVAGNTIIVTSHLEPPTFLCMS 65
DB 5 NDTQFHTSFLGLIGLEVEYHINIGFPFVSYIILAGNAATFVYQDSLHPPYTC 64
OY 66 LCMISGDIISTSMRMLAIFWNSSTIOFDACLLQMFALHSHSGMESTVILMAFDR 125
DB 65 LAMLDISLSTATIPKMLGIFWENIKESIFGYSOMFPIHFYVNESIVAVMAFDR 124
OY 126 YVAICHLRAATVLTLPRTKIGVAANVRGAALMAPLPVFIKQLPFCSNLSHSCYCHQ 185
DB 125 YVAICHLRAATVLTLPRTKIGVAANVRGAALMAPLPVFIKQLPFCSNLSHSCYCHQ 184
OY 186 DWKILACDDIRVNVYGLIYIISAIGDSLISFYLILKTVGL-TREAOAKAFGCV 244
DB 185 GIARLACASIKVIMFGL-GSISLLLDVLLIISIRILKXAPCLPSWBARLALNTCG 243
OY 245 SHVCAVFETVYFGLSNVHRSKRSDPLVILANTILNVPVNPVYGVKTEIKRIQR 304
DB 244 SHIGVILAFSTPAFESFECFGHDIOYIHIFLANLYVVPPLNVPVYGVKTEIKRIRET 303
OY 305 IRLRFVATH 314
DB 304 VLRIFFTDH 313

RESULT 11
OY84_HUMAN STANDARD; PRT; 310 AA.
AC Q9Y5P0;
DT 16-OCT-2001 (Rel. 40, Created)

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FT DOMAIN 160 196 EXTRACELLULAR (POTENTIAL).
 FT TRASNEM 197 220 5 (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRASNEM 238 260 6 (POTENTIAL).
 FT DOMAIN 261 273 EXTRACELLULAR (POTENTIAL).
 FT TRASNEM 280 299 7 (POTENTIAL).
 FT DOMAIN 300 319 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 98 190 BY SIMILARITY.
 FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 319 AA; 35172 MW; 602602RCA96A179F CRC64;

Query Match 28.8%; Score 468; DB 1; Length 319;
 Best Local Similarity 35.6%; Pred. No. 1.3e-28;
 Matches 114; Conservative 63; Mismatches 111; Indels 32; Gaps 9;

QY 8 NEESSAY-FILGL---PGLEAOFWIAFPICSLYLAIVAGNLITIVTEHSHHPM 63
 DB 5 NEESPWGFVLLSHAPHELEKFEVL---TLNMTVLTLGNVLLITLIDSLRHPM 61
 QY 64 IFCLMISGIDILITSSMPRLAIFWENSTTIOFDACLOMFALHSLSGNESTVLAMAF 123
 DB 62 FFLGNLSFDICTTSVPLVDSPFLPORTISFSACAVGMALSPNAGTECLLSMAAF 121
 QY 124 DRVACHELRATVTLRTKIGVAA-VYRGAALMAPLVITKOLPFRSNTLSHYC 182
 DB 122 DRVACHELRATVTLRTKIGVAA-VYRGAALMAPLVITKOLPFRSNTLSHYC 180
 QY 183 LHODVAKLACDDIRVNVVGLIYIISAIGDSLISFYLLIKTVGL-TREAQAKAFG 241
 DB 181 ELIAVAKLACADISIVISKEVNVFLGVPVLEISFYFITTLIRISABEKRVFS 240
 QY 242 TCVSVCVAFIEFYVPEIGLSMVHRFSKRRDS-----PLFVILANITLVPPV 288
 DB 241 TCSAHLTVIVFYEGT---LEFMYGRKRSKDSMGADKEDLSDKILPL-----FVGVTVM 291
 QY 289 LNPYGVGTEKRIORILRL 308
 DB 292 LNPITLIRNKDKVKAARRL 311

RESULT 13
 OL15_MOUSE STANDARD; PRT; 312 AA.
 ID OL15_MOUSE
 AC P23275;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Olfactory receptor 15 (OR3).
 GN OLFR15.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathu; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93028384; PubMed=1384038;
 RA Dione V.E., Hellemann S.F.;
 RA "Spatial pattern of receptor expression in the olfactory epithelium";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8948-8952(1992).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; M84005; AAA39862.1; -
 DR MGD; MG1:106182; OLFR15.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: pf00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Olfaction; Multigene family.
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
 FT TRASNEM 25 48 1 (POTENTIAL).
 FT DOMAIN 49 57 CYTOPLASMIC (POTENTIAL).
 FT TRASNEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRASNEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRASNEM 140 160 4 (POTENTIAL).
 FT DOMAIN 161 200 EXTRACELLULAR (POTENTIAL).
 FT TRASNEM 201 222 5 (POTENTIAL).
 FT TRASNEM 223 236 CYTOPLASMIC (POTENTIAL).
 FT TRASNEM 237 261 6 (POTENTIAL).
 FT DOMAIN 262 272 EXTRACELLULAR (POTENTIAL).
 FT TRASNEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 6 6 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 312 AA; 34333 MW; 8D387EBBF51E132 CRC64;

Query Match 27.1%; Score 440; DB 1; Length 312;
 Best Local Similarity 34.6%; Pred. No. 1.6e-26;
 Matches 113; Conservative 65; Mismatches 123; Indels 26; Gaps 11;

QY 1 MNPVNGNNESSATFILLGL---PGLEAOFWIAFPICSLYLAIVAGNLITIVTEHSH 57
 DB 1 MEVDNSN---SSSGFFILMGVSDHHELIFFAV---ILASYLLTLVGNLTITLLSRDAR 54
 QY 58 LHEPMTIFCLMISGIDILITSSMPRLAIFWENSTTIOFDACLOMFALHSLSGNESTV 117
 DB 55 LHPMTIFCLMISGIDILITSSMPRLAIFWENSTTIOFDACLOMFALHSLSGNESTV 114
 QY 118 LLAFAFRVYVACPLRHATVTLRTKIGVAAV-VYRGAALMAPLVITKOLPFRS 175
 DB 115 LVYVAFDRVYVACPLRHATVTLRTKIGVAAV-VYRGAALMAPLVITKOLPFRS 172
 QY 176 ILSHSYCLHODVAKLACDDIRVNVVGLIYIISAIGDSLISFYLLIKTVGL-T 232
 DB 173 KVDNFELEVPAMIRKLAGDSILNEAVLNGVCTFTVVPVSYILV-SYCFIAQVAKIRS 230
 QY 233 REAQAARFGTCVSHVCAVFIYVPEIGLSMVHR---SKRDSPLVITLANTYLVPPV 289
 DB 231 VEGRRKAFNTCVSHLVVVFLEYG---SAIYGLLPKSSNOSQGRFISLFYSVTIPV 285
 QY 290 NPIYGVGTEKRIORILRLFHVATHAS 316
 DB 286 NPLITLIRNKDKVKAARRL 312

RESULT 14
 OSFL_HUMAN STANDARD; PRT; 314 AA.
 ID OSFL_HUMAN
 AC G95221;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Olfactory receptor 5f1 (Olfactory receptor 11-10) (OR11-10).
 GN OSFL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 68-283 FROM N.A.
 RX MEDLINE=99005533; PubMed=9787077;
 RA Buettner J.A., Glusman G., Ben-Arie N., Ramos P., Lancet D.,

RA Evans G.A.:
 RT "Organization and evolution of olfactory receptor genes on human
 RL chromosome 11.";
 RN Genomics 53:56-68(1998).
 [12]
 RP SEQUENCE OF 68-283 FROM N.A.
 RA Fuchs T., Malécova B., Linhart C., Sharan R., Rhen M., Herwig R.,
 RA Shmulevich D., Elkon R., Steinfach M., O'Brien J.K., Radcliff U.,
 RA Lehnach H., Olander Z., Glusman G., Lancel D., Shamir R.,
 RT "Derog: a practical scheme for deciphering families of genes.";
 RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: AF065863; AAC70017.1; -
 DR EMBL: AF399527; AAK95012.1; -
 DR Genew: HGNC:8343; ORSFL.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 196 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 259 6 (POTENTIAL).
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 5 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 314 AA; 35131 MW; C14A9A35CD76E3A3 CRC64;
 Query Match 26.8%; Score 435.5; DB 1; Length 314;
 Best Local Similarity 32.7%; Pred. No. 3.6e-26;
 Matches 102; Conservative 58; Mismatches 123; Indels 29; Gaps 6;
 OY 8 NESAATYFLIGLPLEAQTALPCLSTVLAIVGNTIYIVTRESLHEPNTFLC 67
 DB 5 NTSLSFEVVLGLADTLEQITLPTVYTLVNGMLLRIDSOQLTPMFLA 64
 OY 68 MLSGIDILISTSMKMLAIEFNFSTTIQFACLQNAIHSIGNESTVLLAMAFDRV 127
 DB 65 NLSFYDVCNSTIIPKMLADLSEKTIISFNGCFLOMFISLATTECLIGLMAIDRYA 124
 OY 128 AICHELRLAIVLTLPRTKIGVAAYVGAALMAPLPEFIKOLPECRSNLSHYCLHODV 187
 DB 125 AICRPLSLTSLMSRTVYKMAAGAPAGILNFMVNTSVHSISFDCSNVIRHFFCDSPPL 184
 OY 188 KTLACDD-----IRVVYGLVYIISAGIDSLTISFVLLIKTYLGL-TREA 235
 DB 185 FTLSSDPTILAESISSIAGINAVGLTLLVLS-----SYTVL--SIFSMSGEG 233
 OY 236 QAKAGTCVSHVCAVFIYVP--FIGLSMVRHSKRSDPLVILLANIYLLVPLVPLNPIV 293

DB 234 KRAEFTCSHLTAITLFTATCTIYLRPSSSYLNDK-----VASFTVYVPLMPLI 289
 OY 294 YGVTKREIRORI 305
 DB 290 YSLRSKEVKKAL 301
 RESULT 15
 OLFA_RAT
 ID OLFA_RAT STANDARD; PRT; 312 AA.
 AC P23273;
 DT 01-NOV-1991 (rel. 20, Created)
 DT 01-NOV-1991 (rel. 20, Last sequence update)
 DE 01-JUL-1993 (rel. 26, Last annotation update)
 OS Olfactory receptor-like protein 114.
 OC Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91191556; PubMed-1840504;
 RA Buck L., Axel R.;
 RT A novel multigene family may encode odorant receptors: a molecular
 RT basis for odor recognition.";
 RL Cell 65:175-187(1991).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: M64391; AAA41754.1; -
 DR PIR: I23701; I23701.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 120 3 (POTENTIAL).
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 158 4 (POTENTIAL).
 FT DOMAIN 159 196 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 197 219 5 (POTENTIAL).
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 260 6 (POTENTIAL).
 FT DOMAIN 261 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 97 N-LINKED (GLCNAc...) (POTENTIAL).
 FT DISULFID 5 BY SIMILARITY.
 SQ SEQUENCE 312 AA; 35718 MW; 08F68546994BA1680 CRC64;
 Query Match 26.8%; Score 434.5; DB 1; Length 312;
 Best Local Similarity 33.5%; Pred. No. 4.2e-26;
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;
 OY 8 NESAATYFLIGLPLEAQTALPCLSTVLAIVGNTIYIVTRESLHEPNTFLC 67
 DB 105 NTSLSFEVVLGLADTLEQITLPTVYTLVNGMLLRIDSOQLTPMFLA 64


```

Db      5  NQTLLEFLGLPIPEYHLLFYALFLAMVLTITIGNLLIIVRLDSHLMPYLFIS 64
QY      68  MLSGIDILISTSPMKMLAIFWPNSTTQFDACILQMFALHSLSGNESTVILAMAFDRYV 127
Db      65  NLSFSDLCPSSVTMPKLNQNMOSQVPSISYTGCLQTLFEMVFGDMESFLVMAVDRTV 124
QY      128  AICHPLRHATVLTLPRTVKIGVAANV-----RGAALMAPLPVFYKOLPECRSNILSHSY 181
Db      125  AICPPLARTTINS---TRPCASLVLLMMLMTFALHTL--LIARLSFCEKNVILHFF 178
QY      182  CLHODVAKLACDDIRVN-----VYGLVIISAGLSLISFSYLLIKTVLGL-TREA 235
Db      179  CDISALTKLSCSDIYVNEIMYIILGGLIITII-----PELLIVMSYVRIFFSILKFPSSIOD 233
QY      236  QAKAFGTCVSHCAVEIFYVPFEGISWVHRSKRDSPLPVILANIYLLVPVLPDIYVG 295
Db      234  IYVSTGSHLSVYTLFGITLFGIYLCF---SGNNSTVKEIMAMKTYVVTPLNPFITIS 291
QY      296  VTKETIRQRIIRL 308
Db      292  LNRDMKRRLIRV 304

```

Search completed: March 26, 2003, 09:53:02
 Job time : 26 secs

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:51:52 ; Search time 87 Seconds

(without alignments)
753.138 Million cell updates/sec

Title: US-09-966-459A-2

Perfect score: 1623

Sequence: 1 MNDPNGNESSATYFILIGL.....KEIRORILRLFHVATHASEP 318

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTIST:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1618	99.7	317	4	08TCB6
2	1516	93.4	317	11	08VG27
3	989	60.9	320	11	08VBV9
4	971.5	59.9	322	11	08VF09
5	918.5	56.6	315	11	08VH05
6	901.5	55.5	312	11	08VH11
7	879.5	54.2	314	11	08VG26
8	877.5	54.1	318	11	08VG23
9	877	54.0	313	11	08VH17
10	871.5	53.7	314	11	08VG22
11	866.5	53.4	317	11	08VH01
12	861.5	53.1	319	11	08VG28
13	858	52.9	317	11	08VH04
14	857.5	52.8	319	11	08VGW0
15	856.5	52.8	319	11	09EQ07
16	856	52.7	317	11	08VEX9

17	844.5	52.0	319	11	08VG29	08VG29 mus musculus
18	842.5	51.9	312	11	08VGX6	08VGX6 mus musculus
19	839.5	51.7	314	11	08VH15	08VH15 mus musculus
20	839	51.7	330	11	08VF07	08VF07 mus musculus
21	838	51.6	316	11	08VG78	08VG78 mus musculus
22	837.5	51.6	317	11	08VGX8	08VGX8 mus musculus
23	835.5	51.5	317	11	08VG09	08VG09 mus musculus
24	832	51.3	312	11	08VH12	08VH12 mus musculus
25	831.5	51.2	314	11	08VG85	08VG85 mus musculus
26	831.5	51.2	319	11	08VG76	08VG76 mus musculus
27	830	51.1	316	11	08VG79	08VG79 mus musculus
28	830	51.1	318	11	08VH16	08VH16 mus musculus
29	828.5	51.0	327	11	08VF28	08VF28 mus musculus
30	827.5	51.0	329	11	08VGX9	08VGX9 mus musculus
31	826.5	50.9	316	11	08VG20	08VG20 mus musculus
32	825.5	50.9	315	11	08VG75	08VG75 mus musculus
33	822.5	50.7	312	11	08VF02	08VF02 mus musculus
34	820	50.5	319	13	09YH55	09YH55 gallus galli
35	818	50.4	315	11	08VG23	08VG23 mus musculus
36	815.5	50.2	314	11	08VH21	08VH21 mus musculus
37	814.5	50.2	313	11	08VG74	08VG74 mus musculus
38	810	49.9	312	11	08VGW2	08VGW2 mus musculus
39	807.5	49.8	321	11	08VH20	08VH20 mus musculus
40	807	49.7	326	11	09WVD9	09WVD9 mus musculus
41	806	49.7	323	11	08VG75	08VG75 mus musculus
42	805.5	49.6	321	11	08VH19	08VH19 mus musculus
43	800	49.3	316	11	09EQ05	09EQ05 mus musculus
44	800	49.3	317	11	08VH13	08VH13 mus musculus
45	798	49.2	318	11	08VH14	08VH14 mus musculus

ALIGNMENTS

RESULT 1
ID 08TCB6 PRELIMINARY; PRT; 317 AA.
AC 08TCB6
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Hypothetical 35.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LUNG;
RC Strusberg R.;
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022401; AAH22401.1; -
KW Hypothetical protein.
SQ SEQUENCE 317 AA; 35271 MW; 8C7293AA7BCA95C CRC64;

Query Match 99.7%; Score 1618; DB 4; Length 317;

Best Local Similarity 100.0%; Pred No. 1.6e-137; Indels 0; Gaps 0;

Matches: 317; Conservative 0; Mismatches 0;

QY	2	MNDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSYTLNAVIGNLTITITVREHSIHP	61
DB	1	MNDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSYTLNAVIGNLTITITVREHSIHP	60
QY	62	MYFLCMLSGIDILISTSSPKKLAIFWENSTTIQDPACILQWFAIHSLSGMSYVLAM	121
DB	61	MYFLCMLSGIDILISTSSPKKLAIFWENSTTIQDPACILQWFAIHSLSGMSYVLAM	120
QY	122	APFRYVAICHPLHARVTLPRYTKIGVAAYVGAALMAPLPEITQLPCCRNIISHSY	181
DB	121	APFRYVAICHPLHARVTLPRYTKIGVAAYVGAALMAPLPEITQLPCCRNIISHSY	180
QY	182	CLHQDVKLACDDIRNVVYGLVITISAGIDLSLISFYLLIKTKVTLGTFRQAQAKG	241

Db 181 CLHODVAKLACDDIRVNVYGLIYISAIGDLSILISFYLIIKTLYGIPREDAKAFG 240
 QY 242 TCVSVCVAVFIETYPETIGLSVNRHSKRSDPLVILANITLVPVLPNIYGVKTKREI 301
 Db 241 TCVSVCVAVFIETYPETIGLSVNRHSKRSDPLVILANITLVPVLPNIYGVKTKREI 300
 QY 302 RORILRLEFHVATHASEP 318
 Db 301 RORILRLEFHVATHASEP 317

RESULT 2

Q8V6Z7 PRELIMINARY; PRT; 317 AA.
 AC Q8V6Z7;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Olfactory receptor MOR18-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY072993; AAL60656.1; -;
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECCEP_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 317 AA; 35463 MW; 5A0E59E229852534 CRC64;

Query Match 93.4%; Score 1516; DB 11; Length 317;
 Best Local Similarity 93.7%; Pred. No. 2,3e-128;
 Matches 296; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 2 MVDNGNESSSTYFLLGLPGLERAGQFWLAPLCSLYILAVLGNLTIIYVTRHSLSHEP 61
 Db 1 MVDNGNESSSTYFLLGLPGLERAGQFWLAPLCSLYILAVLGNLTIIYVTRHSLSHEP 60
 QY 62 MYIFGLMSGDIILISTSSMPKMLAIFWENSTTIQFDACLQMFRAHSLSGMESTVLLAM 121
 Db 61 MYIFGLMSGDIILISTSSMPKMLAIFWENSTTIQFDACLQMFRAHSLSGMESTVLLAM 120
 QY 122 AFDRYVAICHPLRATVLTLPRTYKIGVAAVVGAAALMAPLPVFIKQDPFCRSNLTSHSY 181
 Db 121 AFDRYVAICHPLRATVLTLPRTYKIGVAAVVGAAALMAPLPVFIKQDPFCRSNLTSHSY 180
 QY 182 CLHODVAKLACDDIRVNVYGLIYISAIGDLSILISFYLIIKTLYGIPREDAKAFG 241
 Db 181 CLHODVAKLACDDIRVNVYGLIYISAIGDLSILISFYLIIKTLYGIPREDAKAFG 240
 QY 242 TCVSVCVAVFIETYPETIGLSVNRHSKRSDPLVILANITLVPVLPNIYGVKTKREI 301
 Db 241 TCVSVCVAVFIETYPETIGLSVNRHSKRSDPLVILANITLVPVLPNIYGVKTKREI 300
 QY 302 RORILRLEFHVATHASEP 317
 Db 301 RORILRLEFHVATHASEP 316

RESULT 3
 Q8VBV9 PRELIMINARY; PRT; 320 AA.
 ID Q8VBV9;
 AC Q8VBV9;

DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Olfactory receptor MOR18-2 (Prostate-specific G protein-coupled receptor RALG).
 GN OLF8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY073011; AAL60674.1; -;
 DR EMBL: AF378854; AAL35109.1; -;
 DR MGI: 2157548; Olftr78.
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECCEP_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 320 AA; 35577 MW; 7161ACABF4328959 CRC64;

Query Match 60.9%; Score 989; DB 11; Length 320;
 Best Local Similarity 60.1%; Pred. No. 5,3e-81;
 Matches 184; Conservative 52; Mismatches 68; Indels 2; Gaps 2;

QY 8 NESSATYFLLGLPGLERAGQFWLAPLCSLYILAVLGNLTIIYVTRHSLSHEP 67
 Db 5 NESSATYFLLGLPGLERAGQFWLAPLCSLYILAVLGNLTIIYVTRHSLSHEP 63
 QY 68 MLSGDIILISTSSMPKMLAIFWENSTTIQFDACLQMFRAHSLSGMESTVLLAM 127
 Db 64 MLSGDIILISTSSMPKMLAIFWENSTTIQFDACLQMFRAHSLSGMESTVLLAM 123
 QY 128 AICHPLRATVLTLPRTYKIGVAAVVGAAALMAPLPVFIKQDPFCRSNLTSHSY 187
 Db 124 AICHPLRATVLTLPRTYKIGVAAVVGAAALMAPLPVFIKQDPFCRSNLTSHSY 183
 QY 188 MVLACDDIRVNVYGLIYISAIGDLSILISFYLIIKTLYGIPREDAKAFG 246
 Db 184 MVLACDDIRVNVYGLIYISAIGDLSILISFYLIIKTLYGIPREDAKAFG 243
 QY 247 VCAYFIETYPETIGLSVNRHSKRSDPLVILANITLVPVLPNIYGVKTKREI 306
 Db 244 VCAYFIETYPETIGLSVNRHSKRSDPLVILANITLVPVLPNIYGVKTKREI 303
 QY 307 RLFAVA 312
 Db 304 AMFKIS 309

RESULT 4
 Q8VF09 PRELIMINARY; PRT; 322 AA.
 ID Q8VF09;
 AC Q8VF09;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)

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DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Olfactory receptor MOR18-3.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY072983; AL60646.1;
DR InterPro: IPR002106; AATRNA_1lgase11.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35612 MW; D40302782D4B2FEF CRC64;

Query Match 59.9%; Score 971.5; DB 11; Length 322;
Best Local Similarity 58.5%; Pred. No. 2e-79;
Matches 182; Conservative 58; Mismatches 68; Indels 3; Gaps 3;

OY 1 MANDPNGNESSATYFTLIGLPGLE-EAOFWIAAPLCLYLAVGNLTIIYVTEHSLH 59
DB 8 LIMPNGSLAHPELVGIPGLSGSKHFLAPLPCFNVAVATGNALIIIFIRVERRLH 67
OY 60 EPRATFLCMISGIDILISTSMRKMAIFENSTTIOFDACLOMFAHISLGSMEVTL 119
DB 68 EPRATFLCMISGIDILISTSMRKMAIFENSTTIOFDACLOMFAHISLGSMEVTL 127
OY 120 AMAFDRVAICHPLRHATVTLPRVTRIGVAAYVGAALAPLPVFIKOLPECRNLTSH 179
DB 128 AMAFDRVAICHPLRHATVTLPRVTRIGVAAYVGAALAPLPVFIKOLPECRNLTSH 187
OY 180 SYCHODVMKACDDIRVNVYGLIVTISAIGLDSLISFYLLIKTVLGL-TREAQAK 238
DB 188 SYCHODVMKACDDIRVNVYGLIVTISAIGLDSLISFYLLIKTVLGL-TREAQAK 247
OY 239 AFGTCVSHCAVFIYVYFGLSNMHRFSKRSDPLVILANTYLLVPLNPIYGVKT 298
DB 248 AFGTCVSHCAVFIYVYFGLSNMHRFSKRSDPLVILANTYLLVPLNPIYGVKT 306
OY 299 KEIRORLRL 309
DB 307 KEIRORLRL 317

RESULT 5
OYVH05 PRELIMINARY; PRT; 315 AA.
AC OYVH05;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Olfactory receptor MOR10-1.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]

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RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY072983; AL60646.1;
DR InterPro: IPR002106; AATRNA_1lgase11.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 315 AA; 35157 MW; BAA50EF966E3F0A9 CRC64;

Query Match 56.6%; Score 918.5; DB 11; Length 315;
Best Local Similarity 54.9%; Pred. No. 1.1e-74;
Matches 169; Conservative 64; Mismatches 74; Indels 1; Gaps 1;

OY 3 VDPNGNESSATYFTLIGLPGLE-EAOFWIAAPLCLYLAVGNLTIIYVTEHSLH 62
DB 1 MNSNASQTNHSHFLLTGIPGMPDKNPMWAFGLFTYLLTLLNGCTIIAVKVEGSLHEPM 60
OY 63 YIFLCMISGIDILISTSMRKMAIFENSTTIOFDACLOMFAHISLGSMEVTLAMA 122
DB 61 YIFLCIATLDVSLSMSTPLSMSTIFENFNAPEIPDCACTOMFPIHGGVSGVLVMA 120
OY 123 FDRVAICHPLRHATVTLPRVTRIGVAAYVGAALAPLPVFIKOLPECRNLTSHSYC 182
DB 121 FDRVAICHPLRHATVTLPRVTRIGVAAYVGAALAPLPVFIKOLPECRNLTSHSYC 180
OY 183 LHODVMKACDDIRVNVYGLIVTISAIGLDSLISFYLLIKTVLGL-TREAQAKFG 241
DB 181 LHODVMKACDDIRVNVYGLIVTISAIGLDSLISFYLLIKTVLGL-TREAQAKFG 240
OY 242 TCYVSHCAVFIYVYFGLSNMHRFSKRSDPLVILANTYLLVPLNPIYGVKTKEI 301
DB 241 TCYVSHCAVFIYVYFGLSNMHRFSKRSDPLVILANTYLLVPLNPIYGVKTKEI 300
OY 302 RORLRL 309
DB 301 RORLRL 308

RESULT 6
OYVH11 PRELIMINARY; PRT; 312 AA.
AC OYVH11;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Olfactory receptor MOR7-2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY072977; AL60640.1;
DR InterPro: IPR002106; AATRNA_1lgase11.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 312 AA; 34574 MW; CD233B37733052E5 CRC64;

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	Query Match	55.5%	Score 901.5;	DB 11;	Length 312;	
	Best Local Similarity	53.2%;	Pred. No. 3.8e-73;			
	Matches 165; Conservative	63;	Mismatches 81;	Indels 1;	Gaps 1.	
Oy	1 MAMDVNGNESSATYFYLIGLPGLEAEAOFWLAFLPCLSLYLAVLGNIYYIVRTEHSLHE	60				
	: : : : : : : : : : : : : : : :					
Dd	1 MTPGRLGNSSMSSTFLTSGIPGLEHHMHWISLPICMLMYITSLTGCTLIIFIKTEPSLHE	60				
Oy	61 PWTIYLCMLSGIDILISTSSMPKMAIAWFENSTTIQFDACLLQMFALHSLSGMESTVTLLA	120				
	: : : : : : : : : : : : : : : : : : :					
Dd	61 PYATLSMLALDGLSICTLEPTVLGIETWVGARDISHDACFTOLFIEHCLSTELESSEVLTS	120				
Oy	121 MAFDFRYVAIGHPLRAHYLTLPRTVKIGVAAVVRGAALMAPDPVTKOLPQRSNLTSH	180				
	: : : : : : : : : : : : : : : : : : :					
Dd	121 MAFDFRVACRLAHASILTHTVIIRIGIASIGRSVALFPPEMKLRPPYGCSLVLSHS	180				
Oy	181 YCHADVMKLCCDDIRNVNVVYGLIYISAIGLSDILLSFSYLLIKTTVGL-TREAQAFA	239				
	: : : : : : : : : : : : : : : : : : :					
Dd	181 YCHLBEPVKKACADIKANSITYGMFIYSVGVDSILLILEFYALIRTYSISRARLKTA	240				
Oy	240 FGTGSVCAVEFIYPPIFGTSMVARFRSKRDSPLEVLANTITYLLVPVLANPIYGVKTC	299				
	: : : : : : : : : : : : : : : : : : :					
Dd	241 IATVCASHISAVLTFPTPMIGLSVIRHRFGQAPHLVQVVAGFYVTLPPVMANPIYVSVKTK	300				
Oy	300 EIRORTLRKF 309					
	: : : : : : : : : : : : : : : : : : :					
Dd	301 QTRDRVAAHF 310					
	: : : : : : : : : : : : : : : : : : :					
	RESULT 7					
Oy	08VGZ6 PRELIMINARY; PRT; 314 AA.					
AC	08VGZ6;					
DT	01-MAR-2002 (TREMBLrel. 20, Created)					
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE	Olfactory receptor MOR14-2.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
NCBI_Taxid	-10090;					
LN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Zhang X., Firestein S.J.;					
RT	"The olfactory receptor gene superfamily of the mouse."					
RL	Nat. Neurosci. 0:0-0(2002).					
RN	[2]					
RE	SEQUENCE FROM N.A.					
RA	Adams M.;					
DR	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.					
DR	EMBL; AY072994; AAL60657.1;					
DR	InterPro; IPRO02106; AALRNA_ligase1.					
DR	InterPro; IPRO02376; GPCR_Rhodopsn.					
DR	Pfam; PF00001; Tcm1.1;					
DR	PROSITE; PS00339; AA_TRNA_LIGASE_1; UNKNOW_N_1.					
DR	PROSITE; PS00337; G_PROTEIN_RECIP_F1_1; UNKNOW_N_1.					
DR	PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.					
DR	Receptor.					
SQ	SEQUENCE 314 AA; 35096 MW; 9F1016F8B81A040E9 CRC64;					
	Query Match 54.2%; Score 879.5; DB 11; Length 314;					
	Best Local Similarity 52.6%; Pred. No. 3.6e-71;					
	Matches 163; Conservative 62; Mismatches 82; Indels 3; Gaps 2					
Oy	5 PNGNSSA--TYFIIIGDLGEADQFWLAFLPCLSLYLAVLGNIYYIVRPHSHHEPN	62				
	: : : : : : : : : : : : : : : : : : :					
Dd	2 PPNNSSTAIAPPYFGLTIGLETSHRWISIPPCCLTAINISGSMILFYITRESSLHEPN	61				
Oy	63 YIFCLMLSGIDILISTSSMPKMAIAWFENSTTIQFDACLLQMFALHSLSGMESTVTLLA	122				
	: : : : : : : : : : : : : : : : : : :					
Dd	62 YIFCLMLSTDTGLCGLSTLYVWGIFWTVREISFPACIGOMFFIHGFIMESSVTLVWA	121				
Oy	123 EDRYAICHPLRHAYVLTLPRTVKIGVAAVVRGAALMAPDPVTKOLPQRSNLTSHSTC	182				

[illegible]

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Db      301 IRKRIIOIF 309

RESULT 9
ID      08VH17      PRELIMINARY;      PRT;      313 AA.
AC      08VH17;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Olfactory receptor MOR1-1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang X., Firestein S.J.;
RT      "The olfactory receptor gene superfamily of the mouse.";
RL      Nat. Neurosci. 0:0-0(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Adams M.;
RT      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL: AY072971; AAL60634.1;
DR      InterPro: IPR000276; GPCR_Rhodopsin.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR      PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KM      Receptor.
SQ      SEQUENCE      313 AA; 35682 MW; 39476E03FD201D6C CRC64;

Query Match      54.0%; Score 877; DB 11; Length 313;
Best Local Similarity 51.8%; Pred. No. 6.1e-71;
Matches 158; Conservative 72; Mismatches 73; Indels 2; Gaps 2;

OY      6 NGNSSATYFLLIGLPGLAEQFWLAFLCSLYLIANGLNTIYIVRTEHSLHEPYIF 65
Db      6 NSSAQKATFF LITFQGLERHGHISIPFCSTIYLITGLNLIHAKRTDNLHEPMYF 64
OY      66 LCMISGIDILISTSSMRKLAIFWENSTTIQFACLQMPAHSLSGNESTVLLAMAADR 125
Db      65 LAMALADIGLCISTLPVIGIFWEDAREIGIPACFTQLFHTLSLVESVLLMSRDR 124
OY      126 YVAICHPLRATVLTLPRTKIGVAAVGAALMAPLPVFIKQLPFCRSNLTSLCHQ 185
Db      125 YVAICNPLKSTLTLPRIYKMGISVLSALLILPLPFLIKRHRYSVLAHAYCIHL 184
OY      186 DVMELADDIRVNVVGLIYISALIGDSILISFVLLIKTVLG-LTREQAARFGTCV 244
Db      185 EIMKLACSSIIYVNIYGLFVYACTVGDVSLIFLSTYLLIHAAYLGKRSROERLALNCCI 244
OY      245 SHVCAVFLYVPIGLSNVHRSKRSDPLPVILANIYLLVPPVLPVGVKTKELROR 304
Db      245 SHICAVLFTYPMIGLSLVHRFGHLPRIYHLSYTYLLVPLPLNPIYVSIKTKOIROR 304
OY      305 ILRLP 309
Db      305 IIRKE 309

RESULT 10
ID      08VGZ2      PRELIMINARY;      PRT;      314 AA.
AC      08VGZ2;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Olfactory receptor MOR30-1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang X., Firestein S.J.;
RT      "The olfactory receptor gene superfamily of the mouse.";
RL      Nat. Neurosci. 0:0-0(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Adams M.;
RT      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL: AY072998; AAL60661.1;
DR      InterPro: IPR000276; GPCR_Rhodopsin.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR      PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KM      Receptor.
SQ      SEQUENCE      314 AA; 35577 MW; 71BFEF2F351F669 CRC64;

Query Match      53.7%; Score 871.5; DB 11; Length 314;
Best Local Similarity 50.2%; Pred. No. 1.9e-70;
Matches 153; Conservative 68; Mismatches 85; Indels 1; Gaps 1;

OY      2 MYDPNGSSATYFLLIGLPGLAEQFWLAFLCSLYLIANGLNTIYIVRTEHSLHEP 61
Db      1 MVASSNSSSHLPFMLGIPLENYQFWIAFPFCVMTYVALTGNTIITIRIDHTLHEP 60
OY      62 MYTLCMISGIDILISTSSMRKLAIFWENSTTIQFACLQMPAHSLSGNESTVLLAM 121
Db      61 MYTFLALATDLVLSSTQPKMALIIFSHSELEYNACLIQVFIHAFSSVESGVLTMT 120
OY      122 AFDRTVAICHPLRATVLTLPRTKIGVAAVGAALMAPLPVFIKQLPFCRSNLTSLHSY 181
Db      121 ALDRVAICHPLRATVLTLPRTKIGVAAVGAALMAPLPVFIKQLPFCRSNLTSLHSY 180
OY      182 CLHDDVMAKACDDIRVNVVGLIYISALIGDSILISFVLLIKTVLG-LTREQAARF 240
Db      181 CEHNAVLYKVCADRVNKGIGLFAFVGVGDIVIVISYVMILRAVLRPFGARARAF 240
OY      241 GTCVSHVCAVFLYVPIGLSNVHRSKRSDPLPVILANIYLLVPPVLPVGVKTKEL 300
Db      241 GTCASHVCVLIATFTLPALFTLTHRGHVPVAVHINAFNTLLVPLNPIITGVARKQ 300
OY      301 IIRRLP 309
Db      301 IIRVIRGE 309

RESULT 11
ID      08VH01      PRELIMINARY;      PRT;      317 AA.
AC      08VH01;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Olfactory receptor MOR19-1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang X., Firestein S.J.;
RT      "The olfactory receptor gene superfamily of the mouse.";
RL      Nat. Neurosci. 0:0-0(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Adams M.;
RT      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL: AY072967; AAL60650.1;
DR      InterPro: IPR002106; ATRNA_11gaseit.
DR      InterPro: IPR000276; GPCR_Rhodopsin.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.

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RESULT 14		PRELIMINARY: PRT: 319 AA.	
08VGM0	08VGM0		
AC	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Olfactory receptor MOR30-2.		
OS	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RA	SEQUENCE FROM N.A.		
RP	Zhang X., Firestein S.J.;		
RT	"The olfactory receptor gene superfamily of the mouse.";		
RL	Nat. Neurosci. 0:0-0(2002).		
RM	[2]		
RP	SEQUENCE FROM N.A.		
RA	Adams M.;		
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.		
DR	EMBL: AY073034; AL60697.1;		
DR	InterPro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm1.1		
DR	PROSITE: PS00237; G_PROTEIN_RECIP_F1.1; UNKNOWN_1.		
DR	PROSITE: PS50262; G_PROTEIN_RECIP_F1.2; 1.		
RM	Receptor.		
SO	SEQUENCE 319 AA; 35988 MW; B2DBA1465A063F CRC64;		
Query Match 52.8%; Score 857.5; DB 11; Length 319;			
Best Local Similarity 49.48; Pred. No. 3,5e-69;			
Matches 154; Conservative 67; Mismatches 90; Indels 1; Gaps 1			
OY	1	MMVDNGNESSATYVILGLPGLEAQFMAPLCSLYIAVIGNTIIYVTEHSLEH	60
DB	5	LMASRNSSSHETFTILGIPLENQFVAPFPCMTIVATGNTIIAIRIDITLHE	64
OY	61	PMYTFCLMSGIDILISTSSMPKMAIFENSTTIOFACLLQMEAIHSLSGNESTVLLA	120
DB	65	PMYTLFLMATDVLVSSSTQPKMAILFVHHKIEYHACLLQVFPIHAFSSVSGVLT	124
OY	121	MAFDYVVAICGHLRAVYVTLPRVTKIGVAAVVGAAALAPLVFVKOLPQRSNLSHS	180
DB	125	MALDRVVAICPLKRSSTLTTSAVITLGVAVVRGLMWSPPCFMVSRRPFCNKITPOS	184
OY	181	YCIHDDVKMLACDDIRVNVVGLIYISAIGLDSLISFYLLIKTVGL-TREAQAKA	239
DB	185	YCEHNAVYKLVACADIRVNRNGYGLFAFVSGDIYIVSYVMILRAVLRPSGEARLEA	244
OY	240	FQTCVSHVCANFIFVVPFGLSMVHRESRRDSPLEVILANTIIYLLVPPVLANPIVGVKTK	299
DB	245	FQTCVSHGVITLFLIPALFTFLTRFHGHVPRVHVIMFANVYLLVPPMLNPITIGVRRK	304
OY	300	EIKRRLRLFLHY 311	
DB	305	QIRDRYTRGFCY 316	
RESULT 15			
ID	09EQ07	PRELIMINARY: PRT: 319 AA.	
AC	09EQ07;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	MOR 3/Beta4 (Olfactory receptor MOR1-1).		
OS	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
OX	[1]		

Rp	SEQUENCE FROM N.A.
Rc	STAIN-129SV:
Rx	MEDLINE-20570519; PubMed-11121057;
Ra	Bulger M., Bender M.A., van Doornick J.H., Wetman B., Farrell C.M.,
Ra	Felsenfeld G., Groudine M., Hardison R.;
Rt	*Comparative structural and functional analysis of the olfactory
Rt	receptor genes flanking the human and mouse beta -globin gene
Rt	clusters *;
Rl	Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
Rn	[2]
Rp	SEQUENCE FROM N.A.
Ra	Zhang X., Firestein S.J.;
Rt	"The olfactory receptor gene superfamily of the mouse.";
Rl	Nat. Neurosci. 0:0-0(2002).
Rn	[3]
Rp	SEQUENCE FROM N.A.
Ra	Adams M.;
Rl	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
Rl	EMBL; AF133300; AAC1684.1; -
Rl	EMBL; AY072988; AAL6051.1; -
Dr	InterPro: IPR000276; GPCR_Rhodopsn.
Dr	Pfam: PF00001; Tcm.1; 1.
Dr	PRINTS: PR00237; GPCRRHODOPSN.
Dr	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
Dr	PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
Rv	Receptor.
SQ	SEQUENCE 319 AA; 35979 MW; 87FC0385FD19050A CRC64;
Oy	Query Match 52.8%; Score 856.5; DB 11; Length 319;
	Best Local Similarity 53.6%; Pred. No. 4.3e-69;
	Matches 165; Conservative 53; Mismatches 89; Indels 1; Gaps 1
Dd	1 WVDPGNESSAYVELLIGPLGLEAEAFMAFLCSLYLAIVAGNLITIIYVREHSIAMP 61
	1 MATSSRTVSFTLTGIRGYEEFHHWISIPCFYLIVGITGNCMLIAIVTRDPLRHP 60
Oy	62 MYIFCLMSGLDILISTSSMPKMLALEWNSFTTIOFDACLQMFATISLGMESYVLAM 121
	11 : : : : : : : : :
Dd	61 MYFFLAMSLTFDMASLPMTMSELRVLMISREIQFNICVOMFLHTSFESSVTLAM 120
Oy	122 AEDRVVAATCHPRLAHNTVLLPRVTIKGVAAVVRGALMAPLVFIQLDFECRSNIISHSY 181
	11 : : : : : : : : :
Dd	121 ALDRVVAACHPRLAVTILLPKLIAKGVALRSSLIILPLARLAFFFGSHVLSHY 180
Oy	182 CLHQVMKLACDDIRNVNYGGLVIISAIGDSLISFSYLLIKLVGL-TREAQAKAF 240
	:: :: : : : : : : : : :
Dd	181 CLHQVMIRACADIRNFNVIYGLVITLIMGNDISLGTVLISHSVLKIASSEGRLKAL 240
Oy	241 GTCVSHCAVFETVPYFEGLSNWHRFSKRSDSPLYVIANIYLLVPPVLPPIYGVKTKE 300
	: : : : : :
Dd	241 MTCASHICAVLLIYPMYIGLSIVHFRAKSSPLIHIFMAHIYLLVPPVLPPIYSVKTKQ 300
Oy	301 ITRQRIRL 308
	:
Dd	301 IREGILHL 308

Search completed: March 26, 2003, 09:55:37
Job time : 89 secs

RESULT 15		
09EB007		
ID 09EB007	PRELIMINARY:	PRT: 319 AA.
AC 09EB007;		
DT 01-MAR-2001 (TREMBLrel. 16, Created)		
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE MOR 3 Beta4 (Olfactory receptor MOR17-1).		
OS Mus musculus (Mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
OX NCBI_TaxID=10090;		
RN [1]		